

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 01-16-03
Searcher: Beverly C 4994
Terminal time: 23
Elapsed time:
CPU time:
Total time: 25
Number of Searches:
Number of Databases: 1

Search Site	Vendors
STIC	IG Suite
CM-1	STN
Pre-S	Dialog
N.A. Sequence	APS
A.A. Sequence	Geninfo
Structure	SDC
Bibliographic	DARC/Questel
	Other CGN

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Result No.	Score	Query Match	Length	DB ID	Description
1	2194	100.0	440	22 AAB14623	Saitoella complicata
2	1243	56.7	451	23 ABP83793	Fungal decaprenyl
3	1064	48.5	502	23 ABP83792	Fungal decaprenyl
4	1028.5	46.9	537	23 AAC14997	Rhodotorula minuta
5	999.5	45.5	425	23 AAC14998	Rhodotorula minuta
6	996	45.4	403	23 AAC14999	Rhodotorula minuta
7	902.5	41.1	378	23 AAC021869	Isoprenoid related
8	863	39.3	377	18 ABM30762	Decaprenyl synthas
9	742	33.8	430	22 ABP58466	Drosophila melanog
10	658	30.0	321	21 AAB19412	A straight-chain c
11	658	30.0	321	23 ABB81705	Arabidopsis sp. AT
12	658	28.6	272	23 AAU72775	Arabidopsis tocopher
13	628.5	28.6	272	23 ABP41763	Human ovarian anti
14	561	25.6	297	21 AAB19411	A straight-chain C
15	561	25.6	297	23 ABB81704	Arabidopsis sp. AT
16	561	25.6	297	23 AAU72774	Arabidopsis tocoph
17	451.5	20.6	323	22 AAU34728	E. coli cellular P
18	451.5	20.6	323	22 AAU38141	Salmonella typhi C
19	451.5	20.6	323	23 AAO21873	Isoprenoid related
20	445.5	20.3	329	22 AAO35549	Haemophilus influenzae
21	445.5	20.3	329	23 AAO21874	Isoprenoid related
22	445.5	20.3	333	20 AAY24397	Paracoccus denitri
23	445.5	20.3	335	20 AAY24398	Paracoccus denitri
24	439.5	20.0	335	21 AAB21095	Agrobacterium KPN7
25	410	18.7	323	17 AAR92060	Heptaprenyl diphos
26	409	18.6	320	19 AAW47422	Bacillus stearotherm
27	407.5	18.6	448	22 ABB65155	Drosophila melanog
28	405	18.5	322	22 AAU36438	Pseudomonas aerugi
29	404.5	18.4	325	23 AAO21871	Isoprenoid related
30	402.5	18.3	325	20 AAY01634	A decaprenyl diph
31	398.5	18.2	333	22 AAB75107	Rhodobacter sphaer
32	397.5	18.1	333	23 AAO21866	Isoprenoid related
33	396.5	18.1	410	19 AAW53921	Decaprenyl diphos
34	395.5	18.0	337	23 AAO21867	Isoprenoid related
35	395	18.0	315	23 AAO21868	Decaprenyl diphos
36	395	18.0	315	23 AAO21869	Isoprenoid related
37	395	18.0	348	19 AAW53920	Decaprenyl diphos
38	393.5	17.9	320	23 AAO21870	Propionibacterium
39	378.5	17.3	348	22 AAU51415	Staphylococcus aur
40	371.5	16.9	322	22 AAU37010	Lactococcus lactic
41	368	16.8	319	23 ABB54681	Plasmidum falcip
42	368	16.8	538	21 AAB18168	Staphylococcus aur
43	367.5	16.8	312	22 AAU33819	Listeria monocytog
44	362.5	16.5	321	23 ABB49219	Listeria monocytog
45	357	16.3	326	23 ABB49754	Listeria monocytog

ALIGNMENTS

RESULT 1
AAB74623
ID AAB74623 standard; Protein: 440 AA.
XX
AC AAB74623;
AC
XX
DT 23-MAY-2001 (first entry)
XX
DE Saitoella complicata decaprenyl diphosphate synthase protein SEQ:2.
XX
KW Saitoella complicata; decaprenyl diphosphate synthase; coenzyme Q10;
KW Fungus.
XX
OS Saitoella complicata.
XX
PN WO200114567-A1.
XX
PD 01-MAR-2001.
XX
PP 24-AUG-2000; 2000WO-JP05659.
XX
PR 24-AUG-1999;
XX
PA (KANF) KANERA CORP.
XX
PI Matsuda H, Kawamukai M, Yajima K, Ikenaka Y, Hasegawa J;
PI Takahashi S;
XX
DR WPI; 2001-202937/20.
DR N-PSDB; AAF74893.
PT DNA encoding a protein having decaprenyl diphosphate synthase activity
PT and microorganism for producing coenzyme Q10

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2194	100.0	440	22 AAB14623	Saitoella complicata
2	1243	56.7	451	23 ABP83793	Fungal decaprenyl
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4	1028.5	46.9	537	23 AAC14997	Rhodotorula minuta
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8	863	39.3	377	18 ABM30762	Decaprenyl synthas
9	742	33.8	430	22 ABP58466	Drosophila melanog
10	658	30.0	321	21 AAB19412	A straight-chain c

XX
PS Claim 2; Page 28-30; 32pp; Japanese.

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CC The present invention describes a method for microbiologically producing
coenzyme Q10 at a high efficiency by using a gene of the synthesis of
coenzyme Q10 side chain originating in a fungus belonging to the genus
Saitoella. The present sequence represents the specifically claimed
activity. The protein having decaprenyl diphosphate synthase
can be used for producing coenzyme Q10.

SQ Sequence 440 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
100.0%	2194	22	440	100.0%	2.9e-202		0	0	0
Matches 440;				Best Local Similarity					
1 MASPALRISISSLRSVLTASAPSRLCPTSRSSWAAVASSARLVEDP	60			100.0%					
1 MASPAIRISISSLRSVLTASAPSRLCPTSRSSWAAVASSARLVEDP	60			Best Local Similarity					
61 PNQPLINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQSEGKHIRPLMLMAQA	120			100.0%					
61 PNQPLINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQSEGKHIRPLMLMAQA	120			Best Local Similarity					
121 TEVAKVQGWEKVVEPVNPNEGGLAPPEVINDKPDMMNRSGLTQDCEIEGOTSNTLASQ	180			100.0%					
121 TEVAKVQGWEKVVEPVNPNEGGLAPPEVINDKPDMMNRSGLTQDCEIEGOTSNTLASQ	180			Best Local Similarity					
181 RLLAEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAILAGFLGLGRASVALARL	240			100.0%					
181 RLLAEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAILAGFLGLGRASVALARL	240			Best Local Similarity					
QY 241 RNPVEVIELLATVANLVGEFPMQLNTVDAEATATOETFDYLOQKTYLKTAZTAKSC	300			100.0%					
QY 241 RNPVEVIELLATVANLVGEFPMQLNTVDAEATATOETFDYLOQKTYLKTAZTAKSC	300			Best Local Similarity					
301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			100.0%					
301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			Best Local Similarity					
Db 361 ALFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRALAEEYAKALDAIRTTP	420			100.0%					
Db 361 ALFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRALAEEYAKALDAIRTTP	420			Best Local Similarity					
QY 421 ESPARKALEQTLDRKLVRSTR 440				100.0%					
Db 421 ESPARKALEQTLDRKLVRSTR 440				Best Local Similarity					

SQ Sequence 451 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	451	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 RAVSSASRLVPEPDNPQ---LINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQS	104			Best Local Similarity					
QY 301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			57.2%					
Db 117 BGKHMPLVLIMSQTAITPRQRSNFTPSQMDNPISSPSVLADTNPDLSPLVKSAE	176			Best Local Similarity					
QY 165 KDGEGQTSNLLASORRIEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAIL	224			57.2%					
Db 177 AQYDIFAGD-ENTLPQTQRRAEITELHTASLHDVIDASSETRNAPSONQAGNKGMAIL	235			Best Local Similarity					
QY 225 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	284			57.2%					
Db 236 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	285			Best Local Similarity					
QY 285 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	344			57.2%					
Db 296 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	355			Best Local Similarity					
QY 345 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	404			57.2%					
Db 356 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	415			Best Local Similarity					
QY 405 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 440				57.2%					
Db 416 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 451				Best Local Similarity					

XX
PA (KANEKA CORP.

XX
PI Matsuda H, Kawamukai M, Yajima K, Ikenaka Y;

XX
CC WPI: 2002-5-00765/53.

XX
DR N-PSDB; ABN81605.

XX
PT Microbial production of coenzyme Q10 by transformants transferred with
fungal decaprenyl diphosphate synthase gene, on industrial scale for
application in drugs

SQ Sequence 452 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	452	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 RAVSSASRLVPEPDNPQ---LINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQS	104			Best Local Similarity					
QY 301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			57.2%					
Db 117 BGKHMPLVLIMSQTAITPRQRSNFTPSQMDNPISSPSVLADTNPDLSPLVKSAE	176			Best Local Similarity					
QY 165 KDGEGQTSNLLASORRIEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAIL	224			57.2%					
Db 177 AQYDIFAGD-ENTLPQTQRRAEITELHTASLHDVIDASSETRNAPSONQAGNKGMAIL	235			Best Local Similarity					
QY 225 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	284			57.2%					
Db 236 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	285			Best Local Similarity					
QY 285 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	344			57.2%					
Db 296 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	355			Best Local Similarity					
QY 345 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	404			57.2%					
Db 356 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	415			Best Local Similarity					
QY 405 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 440				57.2%					
Db 416 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 452				Best Local Similarity					

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SQ Sequence 453 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	453	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 RAVSSASRLVPEPDNPQ---LINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQS	104			Best Local Similarity					
QY 301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			57.2%					
Db 117 BGKHMPLVLIMSQTAITPRQRSNFTPSQMDNPISSPSVLADTNPDLSPLVKSAE	176			Best Local Similarity					
QY 165 KDGEGQTSNLLASORRIEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAIL	224			57.2%					
Db 177 AQYDIFAGD-ENTLPQTQRRAEITELHTASLHDVIDASSETRNAPSONQAGNKGMAIL	235			Best Local Similarity					
QY 225 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	284			57.2%					
Db 236 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	285			Best Local Similarity					
QY 285 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	344			57.2%					
Db 296 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	355			Best Local Similarity					
QY 345 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	404			57.2%					
Db 356 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	415			Best Local Similarity					
QY 405 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 440				57.2%					
Db 416 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 453				Best Local Similarity					

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PT Microbial production of coenzyme Q10 by transformants transferred with
fungal decaprenyl diphosphate synthase gene, on industrial scale for
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SQ Sequence 454 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	454	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 RAVSSASRLVPEPDNPQ---LINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQS	104			Best Local Similarity					
QY 301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			57.2%					
Db 117 BGKHMPLVLIMSQTAITPRQRSNFTPSQMDNPISSPSVLADTNPDLSPLVKSAE	176			Best Local Similarity					
QY 165 KDGEGQTSNLLASORRIEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAIL	224			57.2%					
Db 177 AQYDIFAGD-ENTLPQTQRRAEITELHTASLHDVIDASSETRNAPSONQAGNKGMAIL	235			Best Local Similarity					
QY 225 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	284			57.2%					
Db 236 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	285			Best Local Similarity					
QY 285 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	344			57.2%					
Db 296 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	355			Best Local Similarity					
QY 345 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	404			57.2%					
Db 356 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	415			Best Local Similarity					
QY 405 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 440				57.2%					
Db 416 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 454				Best Local Similarity					

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CC WPI: 2002-5-00765/53.

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DR N-PSDB; ABN81605.

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PT Microbial production of coenzyme Q10 by transformants transferred with
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application in drugs

SQ Sequence 455 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	455	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 RAVSSASRLVPEPDNPQ---LINPLNLVPEMSNLTSNTRSLIGSGHPSLTDYAKYYQS	104			Best Local Similarity					
QY 301 RASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATDGLKPGADLQLGLATAP	360			57.2%					
Db 117 BGKHMPLVLIMSQTAITPRQRSNFTPSQMDNPISSPSVLADTNPDLSPLVKSAE	176			Best Local Similarity					
QY 165 KDGEGQTSNLLASORRIEITEMIHASSLHDVIDASSETRNAPSONQAGNKGMAIL	224			57.2%					
Db 177 AQYDIFAGD-ENTLPQTQRRAEITELHTASLHDVIDASSETRNAPSONQAGNKGMAIL	235			Best Local Similarity					
QY 225 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	284			57.2%					
Db 236 AGDFLGLGRASVALARLNPEVIELLATVANLVGEFPMQLNTVDAEATATOETFDY	285			Best Local Similarity					
QY 285 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	344			57.2%					
Db 296 LQKTYLKTAZLAKSCRASALIGGATPEVADAAYAGRNLGLAQIVDMDLYVSAATD	355			Best Local Similarity					
QY 345 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	404			57.2%					
Db 356 GKPGADLQGLATPAJFWAKHHAELGMKIKFSDFDVERARELVEKSDSLKEKRAL	415			Best Local Similarity					
QY 405 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 440				57.2%					
Db 416 AEBYAOKALDAIRTPESPARKALEQTLDRKLVRSTR 455				Best Local Similarity					

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SQ Sequence 456 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
56.7%	2143	23	456	57.2%	1.2e-110		0	0	0
Matches 261;				Best Local Similarity					
1 MRARTVSASGLI---LSSTTSPSICWQCLRDLSNQVOIHVRKYHPTRKDVSPG	56			57.2%					
Db 57 R									

QY	273	ENTA-----TOETFDYLQKTYLKLTLASLIAKSRRASALGGATPE-----V 313	Db	163	UTKDGEIEGOTSNILASQRRAEITEMIHAASLHIDDVIDASETRRNAPSGNQAFGGKNA 222
Db	350	ESNASGSKEVAVRILTPFEHYMKKTYLKTLASLIAKSRRASALGGATPE-----V 409	Db	135	L----DSMPSTSNVPSQRRAEITEMIHAASLHIDDVIDASETRRNAPSGNQAFGGKNA 190
QY	314	ADAYAYAGRNLGAFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGL 372	Db	470	QMILRKFENGEVETARNLVRKSAGPEKTVKLAEKHALAMEALQGLPESDAREALEGLT 529
Db	410	KOJAYSGRNGLGAFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGL 469	Db	410	KOJAYSGRNGLGAFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGL 469
QY	373	PMTKRKFSDPGVERARLVEKSDGLEKTRALAEEYAOKALDAIRTPESPARKALEQLT 432	Db	223	ILAGDFTLGRASVALRNPBEVETLAVTANLYVEGETMOLKNTVDDEATEA----- 276
Db	470	QMILRKFENGEVETARNLVRKSAGPEKTVKLAEKHALAMEALQGLPESDAREALEGLT 529	Db	191	VLGDDFLLARSLYLSRLGSNEVWLVASLAVLNVEGETMOLKNTVDDEATEA----- 276
QY	433	DKVLTCSR 440	Db	530	KTVLNRTK 537
RESULT 5			QY	383	GDRVERRELVEKSDGEKTRALAEEYAOKALDAIRTPESPARKALEQLTDKVLTCSR 440
ID	AA014998	standard; Protein; 425 AA.	Db	368	GDVETARNLVRKSAGPEKTVKLAEKHALAMEALQGLPESDARIALLEGITKTVLNRTK 425
AC	AA014998;		Db	308	LGIASFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGLGPMIKRKFSDP 382
XX			QY	324	LGIAFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGLGPMIKRKFSDP 382
DT	08-AUG-2002	(first entry)	Db	248	AHVRLLPEIETHYMKKTYLKTLASLIAKSRRASALGGATPE-----V 323
XX			QY	277	--TOETFDYLQKTYLKLTLASLIAKSRRASALGGATPE-----VADAAYAGRN 323
DE	Rhodotorula minuta decaprenyl diphosphate synthase 2.		Db	248	AHVRLLPEIETHYMKKTYLKTLASLIAKSRRASALGGATPE-----V 323
XX	Fungi; decaprenyl diphosphate synthase; enzyme; high-yield fermentation; coenzyme Q10 production.		QY	308	LGIASFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGLGPMIKRKFSDP 382
KW			Db	308	LGIASFQVDDMLDYTVSATDGRPA-GADQLGLATAPALFAWKHAEGLGPMIKRKFSDP 382
XX	Rhodotorula minuta.		QY	383	GDRVERRELVEKSDGEKTRALAEEYAOKALDAIRTPESPARKALEQLTDKVLTCSR 440
OS			Db	368	GDVETARNLVRKSAGPEKTVKLAEKHALAMEALQGLPESDARIALLEGITKTVLNRTK 425
XX	W0200240682-A1..		RESULT 6		
PN			ID	AA014999	standard; Protein; 403 AA.
XX			AC	AA014999;	
PD	20-NOV-2000; 20000JP-0352940.		XX		
XX			DT	08-AUG-2002	(first entry)
PD	23-MAY-2002.		XX		
XX			DE	Rhodotorula minuta decaprenyl diphosphate synthase 3.	
PA	(KANF) KANEKA CORP.		XX		
XX			KW	Fungi; decaprenyl diphosphate synthase; enzyme; high-yield fermentation; coenzyme Q10 production.	
PF	20-NOV-2001; 2001WO-JP10119.		XX		
XX			OS	Rhodotorula minuta.	
PN	W0200240682-A1..		XX		
XX			PR	20-NOV-2000; 20000JP-0352940.	
XX			XX		
PR	20-NOV-2001; 2001WO-JP10119.		PA	(KANF) KANEKA CORP.	
XX			XX		
PR	20-NOV-2000; 20000JP-0352940.		PI	Matsuda H, Kawamukai M, Yajima K, Ikenaka Y;	
XX			XX		
PA	(KANF) KANEKA CORP.		DR	W0I; 2002-427097/45.	
XX			DR	N-PSDB; AAL42942.	
XX			XX		
PT	Decaprenyl diphosphate synthase gene of Rhodotorula origin for PT efficient preparation of coenzyme Q10 -		PT	Decaprenyl diphosphate synthase gene of Rhodotorula origin for PT efficient preparation of coenzyme Q10 -	
CC	Decaprenyl diphosphate synthase gene of Rhodotorula origin for PT efficient preparation of coenzyme Q10 -		PT	Decaprenyl diphosphate synthase gene of Rhodotorula origin for PT efficient preparation of coenzyme Q10 -	
CC	The invention comprises the amino acid and coding sequences of fungal (Rhodotorula minuta) decaprenyl diphosphate synthase DNA and protein sequences are useful for the efficient, high-yield fermentative production of coenzyme Q10 - for pharmaceutical use. The present amino acid sequence represents a Rhodotorula minuta decaprenyl diphosphate synthase enzyme.		XX	Claim 19; Page 44-46; 50pp; Japanese.	
CC			PS	Claim 19; Page 44-46; 50pp; Japanese.	
CC			XX		
CC			CC	The invention comprises the amino acid and coding sequences of fungal (Rhodotorula minuta) decaprenyl diphosphate synthase enzymes. The fungal decaprenyl diphosphate synthase DNA and protein sequences are useful for the efficient, high-yield fermentative production of coenzyme Q10 - for pharmaceutical use. The present amino acid sequence represents a Rhodotorula minuta decaprenyl diphosphate synthase enzyme.	
SQ	Sequence 425 AA;		CC		
Query Match	45.5%; Score 999; DB 23; Length 425;		SQ	Sequence 403 AA;	
Best Local Similarity	53.9%; Pred. No. 3.3e-87;		Query Match	45.4%; Score 996; DB 23; Length 403;	
Matches	221; Conservative 66; Mismatches 85; Indels 46; Gaps 10;		Best Local Similarity	53.4%; Pred. No. 5.9e-87;	
Db	18	PNAINTTDPDQLGVNGENPLNSLRSRNVQALIGGSPALDTIAYKIVQASEKGKIRPMVILMS 77	Db	135	L----DSMPSTSNVPSQRRAEITEMIHAASLHIDDVIDASETRRNAPSGNQAFGGKNA 190
QY	119	QATE-VAKTQVQGVKVVVE-----PVNEG-----APPVLNDKNP-BMMNRSGP 162	QY	65	LIINPLNLVGPMENSNLTSNRLSISLGGHPSLDTVAKYVYSEKGKIRPMVILMAQATE-V 123
Db	78	QATNGLAB--GREBRSKELSGRSQKQDPSRSINDPLVKADRLBLINNSNPSSFAASSSSP 134	Db	2	IFDPLQLGVNGENPLNSLRSRNVQALIGGSPALDTIAYKIVQASEKGKIRPMVILMSQATNL 61

Qy	124 APKVQGWEKUVV-----PVNEGLI-APPEVLNDRNP-DMMNMRSGLPLTKDGE 168	Query Match 41-1%; Score 902.5; DB 23; Length 378;
Db	62 AP---GFEERKLELSGRKQTDPSPRSINDPLEVKADBILNDNSNPSSFAASSSPS---D 114	Best Local Similarity 50.8%; Pred. No. 5.4e-78; Mismatches 60; Gaps 3;
Qy	169 IEGOTSNILASORRIALAEITEMIHAASLHDDVIDASETRRNAPSGNQAFGNKMAILAGDF 228	Matches 190; Conservative 60; Mismatches 97; Indels 27;
Db	115 SMPSTSIVLPSPSRRLAEITEMIHAASLHDDVIDAGMARRAQASAAFGNKKISVLGGDF 174	
Qy	229 IIGRASVALARLNPEVIELLATVIANLVSEGFMQLNTVDDAIERTA-----T 277	
Db	175 LLARASLYSLRSNEVVELVAVSVLNLVSEGVMQIKG---NAPEENASGSKEVAVHRLT 231	Qy 67 NPLNLVGPMENSNLTSNIRSLLGSGHPSLIDTVAKYVYQSEGEKHIRPLMVJIMAOTAVEVAPK 126
Qy	278 QETFDYLLQKTYLKTTASLIASKRASALLGATPE-----VADAAAYAVGRNIGLAFO 329	Db 32 NASHIJKNELEQISPGIRQMINSNSFLEBGSKYTTIAQQKMRBSVLVLMSKATSLCHG 91
Db	232 PEIFEHYMKCTYLKTTASLIASKRASALLGATPE-----VADAAAYAVGRNIGLAFO 291	Qy 127 VQGMWKVVEVPVNNEGLAPPEVINDXNPDMNNMRSGPLTKDGEIEQTSNLASQRRAEI 186
Qy	330 IVDDMLDVTYSATDLGKPA-GDLQLGLATAPALFWKHHAEGLPMIKRKPSDPGVERA 388	Db 92 ID-----RSVVGDKYTDODDLRS-----FSTGQTLPSQRLAQI 125
Db	292 LVDDLDFTATAQFGKPSQGDLKIGLATAFLAFLYAWEEFPBMGNTLRENEGDVETA 351	Qy 187 TEMIIHASLLEHDVDASTEVRNAPSGNQAFGNKMAILAGDFLLGRASVALARLNPEV 246
Qy	389 RELVEKSDGLEKTRALAEEYAKALDARTPESPARKALEFQLTDKVLTRSR 440	Db 126 TEMIIHASLLEHDVDAHNTVRGSSSNVAFGNRSILAGNFILARASTAMARLNPOV 185
Db	352 RNLVRKSAGPERKTVKLAEKHALAMEAALQGLPESDAREALPGLTKTVLNRTK 403	Qy 247 ELLATVANLYVEGFMLQKNTVDDAIEATATQETFDYVLOKTYLKTTASLIASKRASALL 306
RESULT 7		Db 186 ELLATVANLYVEGFMLQKNTVDDAIEATATQETFDYVLOKTYLKTTASLIASKRASALL 244
ID AAO21869	standard; Protein; 378 AA.	Qy 307 GGATPVEDAYAYGRNLGLAFOIYUDDMLDVTYSATDLGKPGAGDLQLGLATAPALFWK 366
AC AAO21869;		Db 245 QCSPPTVATAAEYGRCIGTAFOLMDDVLDYTSKDTLGKAAGADLKGLGLATAPVLFANK 304
DT 13-SEP-2002	(first entry)	Qy 367 HHAELGPMIKRKFSQDGDVVERAELVEKSQGLEKTRALAEEYAKALDARTFPPESPARK 426
XX		Db 305 KYPELGAMIVNRFHNPDSQDQRARSLSVCTDAEQTITWAEYIKAKDSLCLPDSPARK 364
DE AAO21869		Qy 427 ALEQITDVKVLTCSR 440
KW		Db 365 ALFALADKVITRKK 379
XX		RESULTS 8
XX		AAW30762
AC		ID AAW30762 standard; Protein; 377 AA.
XX		AAW30762;
DT		XX 12-MAR-1998 (first entry)
XX		DE Decaprenyl synthase.
DE Isoprenoid related protein sequence SEQ ID No 47.		XX Decaprenyl synthase gene; heterogenic ubiquinone production; KW transferase; mitochondrial; yeast; hexaprenyl diphosphate; KW modification; genetic engineering.
KW Isoprenoid; CoQ(10); 1-deoxyxylose-5-phosphate synthase; DXS; DDS; XX Schizosaccharomyces pombe.		OS Schizosaccharomyces pombe.
KW decaprenyl diphosphate synthase.		XX JP019173076-A.
XX Rhodobacter capsulatus.		XX 08-JUL-1997.
OS WO200226933-A2.		XX PD 27-DEC-1995;
XX PN 04-APR-2002.		XX 95JP-0351243.
XX PD 28-SEP-2001; 2001WO-US30329.		XX PR 27-DEC-1995;
XX PR 29-SEP-2000; 2000US-2316580P.		XX 95JP-0351243.
XX PA (CRGI) CARGILL INC.		XX (ALPH-) ALPHA SHOKUHN KK.
XX PI Gokarn R, Jessen H, Zidwick MJ;		XX PA JP019173076-A.
XX DR 08-JUL-1997.		XX DR WPI; 1997-397034/37.
XX WPI; 2002-416480/44.		XX DR N-PSDB; AAT191893.
XX Substantially pure polypeptides having e.g.,		XX PT New method for heterogenic ubiquinone production - allows the side chain of ubiquinone to be freely modified by genetic engineering methods
PT 1-deoxyxylose-5-phosphate synthase activity, useful for the		XX PT
PR production of isoprenoids, especially CoQ(10)		XX CC transition sequence of mitochondrial Saccharomyces cerevisiae
XX Disclosure: Fig 14; 246pp; English.		CC hexaprenyl diphosphate synthase structural gene Cog1 to heterogenic prenyl transferase gene and expressing the resultant fused gene. The
CC		CC new method has been developed for the formation of heterogenic prenyl
CC		CC transition sequence of mitochondrial Saccharomyces cerevisiae
CC		CC hexaprenyl diphosphate synthase gene and expressing the resultant fused gene. The
CC		CC new method has been developed for the formation of heterogenic prenyl
CC		CC transition sequence of mitochondrial Saccharomyces cerevisiae
CC		CC hexaprenyl diphosphate synthase structural gene Cog1 to heterogenic prenyl transferase gene and expressing the resultant fused gene. The
Sequence 378 AA;		CC
SQ		CC

PD 26-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US10368.
 PR 15-APR-1999; 99US-0122899.
 PR 30-JUL-1999; 99US-0146461.
 XX
 PA (CALGENE) CALGENE LLC.
 XX
 PI Savidge B, Lassner MW, Weiss JD, Post-Bittenmiller D;
 XX
 DR WPI; 2000-647519/62.
 DR N-PSDB; AAC1900
 XX
 PT An isolated nucleic acid sequence encoding prenyltransferase used to
 PT transform plant cells to increase the production of tocopherols -
 XX
 PS Claim 6; Fig 1; 114pp; English.
 XX
 CC The present sequence represents a prenyltransferase. The specification
 CC describes prenyltransferases designated AtPT1, AtPT2, AtPT3, AtPT4,
 CC AtPT5, AtPT6, AtPT7, AtPT8, AtPT9, AtPT10, AtPT11, and AtPT12. The
 CC biosynthesis of alpha-tocopherol in higher plants involves the
 CC condensation of homogentisic acid and phytolpyrophosphate to form
 CC 2-methyl-6-phytylbenzoquinone, which can form various tocopherols. The
 CC prenyltransferase polynucleotides are useful in transforming host cells
 CC to alter the expression of prenyltransferase in these cells. The
 CC transformed cells are used in the production of tocopherols which are
 CC of use in the pharmaceutical industry as antioxidants and also in the
 CC food industry as nutritional supplements.
 XX
 SQ Sequence 321 AA;
 Query Match 30.0% Score 658; DB 21; Length 321;
 Best Local Similarity 42.0%; Pred. No. 1.Se-54;
 Matches 150; Conservative 64; Mismatches 93; Indels 50; Gaps 5;
 Qy 92 PSLDTVAKYYVS--EGKHIRPLMVLUMAQTAEVAPKVGNEKVVVPVNEGGLAPEVLN 149
 Db 7 PRLASAAEYFFRGVQSKQRFRSTILLIMATANV-----RVEALI 47
 Qy 150 DKNPDMNNMRSGPLTKDGEIGEOTSNTLASQRRAETEMIHAASLHDDVIDASETRN 209
 Db 48 GSTDIV-----TSELVRORGIAETEMTHASLHDDVIDADTRRG 91
 Qy 210 AMSGQNAGKNAILLAGPFLGRASVALARLNPEVLLAVIANVEGEMOLKNTVD 269
 Db 92 VGSLNVMGNKNSVLAGDELLSRACGALAALKNTEVALLAVELVTGETMEITS--- 148
 Qy 270 DATEATAATQETDYDYLKTYLKUTASLIAKSRSALGGATEPEVADAYGRNLGIAFO 329
 Db 149 ---STEQRYSNDYIMORTYTTASYLTSNSCAVAVITGQTAEVIAFETGRNLGIAFO 204
 Qy 330 IVDDMLDVTYSATDLGKPGADLQLGLATAPALFANKHAEIGPMIKRKFSDPGVERAR 389
 Db 205 LDDDLDEFTGTSASLGKGSLSDIRHGVTAPILFAMEBFPQVEKDPRNVDIAL 264
 Qy 390 ELYVEKSGOLEKTRALAREYQAQLADDARTFPESP----ARKALBLLTDKVLTTRSR 440
 Db 265 EYLGKSKGIORARELAMEHANIAAAAIGSLPPTDNEDVKRSRALIDLTHRVTRNK 321
 RESULT 11
 ID ABB81705 standard; Protein; 321 AA.
 XX
 AC ABB81705;
 XX
 DT 16-AUG-2002 (first entry)
 DE Arabidopsis sp. AtPT8.
 XX
 KW Prenyltransferase; PTS; isoprenoid; Synechocystis; Arabidopsis; corn;

KW rice; wheat; leek; canola; cotton; tomato; biosynthetic flux;
 KW tocopherols; AtPT8; polytransferase.
 XX
 OS Arabidopsis sp.
 XX
 PN WO200233060-A2.
 XX
 PD 25-APR-2002.
 XX
 PI 12-OCT-2001; 2001WO-US42673.
 XX
 PR 14-OCT-2000; 2000US-0688071.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Lassner MW, Savidge B, Weiss JD, Mitsky TA, Post-Bittenmiller MA;
 PI Valentini HB;
 XX
 DR N-PSDB; ABQ62170.
 XX
 WPI; 2002-463312/49.
 XX
 PT Novel nucleic acid sequences encoding prenyltransferase derived from
 PT eukaryotic and prokaryotic sources useful for producing plants and
 PT seeds with altered tocopherol content and compositions
 XX
 PS Example 1; Fig 2; 148pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid sequence encoding
 CC a prenyltransferase (PTS). The nucleic acid construct of the invention is
 CC useful for altering isoprenoid content and for producing an isoprenoid
 CC compound of interest in a host cell, such as Synechocystis sp., or a
 CC plant cell obtained from Arabidopsis, corn, rice, wheat, leek, canola,
 CC cotton or tomato. The construct is also useful for increasing
 CC biosynthetic flux in a host cell toward production of isoprenoid
 CC compound such as tocopherol and tocotrienol. The polynucleotide is useful
 CC for producing plants and plant parts, such as seeds, enriched in
 CC tocopherols. The sequence shown represents Arabidopsis sp. AtPT8, a
 CC prenyltransferase identified in the invention.
 XX
 SQ Sequence 321 AA;
 Query Match 30.0%; Score 658; DB 23;
 Best Local Similarity 42.0%; Pred. No. 1.5e-54;
 Matches 150; Conservative 64; Mismatches 93; Indels 50; Gaps 5;
 Qy 92 PSLDTVAKYYVS--EGKHIRPLMVLUMAQTAEVAPKVGNEKVVVPVNEGGLAPEVLN 149
 Db 7 PKLASAAEYFFRGVQSKQRFRSTILLIMATANV-----RVEALI 47
 Qy 150 DKNPDMNNMRSGPLTKDGEIGEOTSNTLASQRRAETEMIHAASLHDDVIDASETRN 209
 Db 48 GSTDIV-----TSELVRORGIAETEMTHASLHDDVIDADTRRG 91
 Qy 210 AMSGQNAGKNAILLAGPFLGRASVALARLNPEVLLAVIANVEGEMOLKNTVD 269
 Db 92 VGSLNVMGNKNSVLAGDELLSRACGALAALKNTEVALLAVELVTGETMEITS--- 148
 Qy 270 DATEATAATQETDYDYLKTYLKUTASLIAKSRSALGGATEPEVADAYGRNLGIAFO 329
 Db 149 ---STEQRYSNDYIMORTYTTASYLTSNSCAVAVITGQTAEVIAFETGRNLGIAFO 204
 Qy 330 IVDDMLDVTYSATDLGKPGADLQLGLATAPALFANKHAEIGPMIKRKFSDPGVERAR 389
 Db 205 LDDDLDEFTGTSASLGKGSLSDIRHGVTAPILFAMEBFPQVEKDPRNVDIAL 264
 Qy 390 ELYVEKSGOLEKTRALAREYQAQLADDARTFPESP----ARKALBLLTDKVLTTRSR 440
 Db 265 EYLGKSKGIORARELAMEHANIAAAAIGSLPPTDNEDVKRSRALIDLTHRVTRNK 321
 RESULT 12
 ARU72755 standard; Protein; 321 AA.
 ID AAU72755

Search completed: January 16, 2003, 09:46:48
Job time : 58 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	445.5	20.3	333	4	US-09-025-819-29 Sequence 29, Appli
2	445.5	20.3	333	4	US-09-025-819-29 Sequence 29, Appli
3	439.5	20.3	333	4	US-09-025-819-29 Sequence 29, Appli
4	439.5	20.0	335	4	US-09-025-819-29 Sequence 2, Appli
5	409	18.6	320	3	US-09-025-819-29 Sequence 6, Appli
6	409	18.6	320	4	US-09-025-819-29 Sequence 6, Appli
7	397.5	18.1	325	3	US-09-025-819-29 Sequence 2, Appli
8	346	15.8	357	4	US-09-025-819-29 Sequence 325, Ap
9	336.5	15.3	325	4	US-09-025-819-29 Sequence 2, Appli
10	336.5	15.3	325	4	US-09-025-819-29 Sequence 2, Appli
11	283	12.9	393	3	US-09-025-819-29 Sequence 28, Appli
12	280	12.8	393	3	US-09-025-819-29 Sequence 27, Appli
13	278	12.7	393	3	US-09-025-819-29 Sequence 2, Appli
14	278	12.7	393	3	US-09-025-819-29 Sequence 14, Appli
15	278	12.7	393	3	US-09-025-819-29 Sequence 16, Appli
16	278	12.7	393	3	US-09-025-819-29 Sequence 18, Appli
17	278	12.7	393	3	US-09-025-819-29 Sequence 20, Appli
18	278	12.7	393	3	US-09-025-819-29 Sequence 22, Appli
19	278	12.7	393	3	US-09-025-819-29 Sequence 24, Appli
20	278	12.7	393	3	US-09-025-819-29 Sequence 26, Appli
21	278	12.7	393	3	US-09-025-819-29 Sequence 29, Appli
22	278	12.7	393	3	US-09-025-819-29 Sequence 30, Appli
23	278	12.7	393	3	US-09-025-819-29 Sequence 31, Appli
24	278	12.7	393	3	US-09-025-819-29 Sequence 32, Appli
25	278	12.7	393	3	US-09-025-819-29 Sequence 33, Appli
26	274	12.5	393	3	US-09-025-819-29 Sequence 34, Appli
27	264	12.0	385	3	US-09-025-819-29 Sequence 12, Appli

Query Match 20.3%; Score 445.5; DB 4; Length 333;
 Best Local Similarity 30.3%; Pred. No. 4.5e-35; Matches 120; Conservative 30.3%; Mismatches 25; Indels 87; Gaps 9; Gaps -GNSHV 76

Db 62 NQPLINPLNIVGPE---MSNLTRNIRSLLGSGI-PSLDTVAKYVVSSEGKHLRPLMVL 116
 Qy 177 LASQRRAETEMIHAASLLHDVIDASERTRRNAPSGNQAFGNKMAILAGDFILGRASVA 236
 Db 4 NENVKPLDLSVELLAGMDRNRNALIREMRSRAPHPIPEVTALVAGGRKLRLPMLV 62
 Qy 117 MAQATEVAKVQGNWKRUVVEPVNVGLAPPVELNDKNPDMMNNRSGPLTKDGIEGOTNSI 176

Db 63 -----AAARLCGQ-----GNSHV 76
 Db 132 MADTSMQVMRLLANASATIAEGVLQL-----TAQDVSTTDTDVQIVRGKTA 181
 Qy 294 SLIAKSCRASALIGGATPEVADAYAAYGRNLGLAQFOIVDDMLDYTVATDGGPKPAGDLO 353
 Db 182 ALPSAATEAGVAGADPAVQQALFDYGDALGIAFQIVDDMLDYTVATDGGPKPAGDLO 241
 Qy 354 LGLATAPALFA-----WGHHAELGPMPKRFSDPGVERARLVEKGLEKTR 402
 Db 242 ERKLTLPVKIKARADEAERAFWER-----TIGQRODEADLATEILRRREALEAR 295
 Qy 403 ALABEYAKQKALDAIRTPESPARALEQITDKLIR 438
 Db 296 ADAIAWAGRAKKAALQAAPDQPPLRRLADLFVUSR 331

RESULT 2

US-09-808-126-29
 Sequence 29, Application US/09808126
 Patent No. 6410280
 GENERAL INFORMATION:
 APPLICANT: Obata, Shusei

Nishino, Tokuko
 Koyama, Taneotsuhi
 Sato, Yoshihiro

TITLE OF INVENTION: DECARRENYL DIPHOSPHATE SYNTHETASE GENE
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:

ADDRESSEE: KENYON & KENYON
 STREET: 1500 K Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/808, 126
 FILING DATE: 08-May-2001
 FILING CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/025, 819

ATTORNEY/AGENT INFORMATION:
 NAME: Khalilian, Houli
 REGISTRATION NUMBER: 39, 546
 REFERENCE/DOCKET NUMBER: 10235/2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-220-4200
 TELEFAX: 202-220-4201
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:

RESULT 3

US-09-803-951-29
 Sequence 29, Application US/09803951
 Patent No. 6413761
 GENERAL INFORMATION:
 APPLICANT: Obata, Shusei

Nishino, Tokuko
 Koyama, Taneotsuhi
 Sato, Yoshihiro

TITLE OF INVENTION: DECARRENYL DIPHOSPHATE SYNTHETASE GENE
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:

ADDRESSEE: KENYON & KENYON
 STREET: 1500 K Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/803, 951
 FILING DATE: 13-Mar-2001
 FILING CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/025, 819
 ATTORNEY/AGENT INFORMATION:
 NAME: Khalilian, Houli
 REGISTRATION NUMBER: 39, 546
 REFERENCE/DOCKET NUMBER: 10235/2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-220-4200
 TELEFAX: 202-220-4201
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:

Query Match 20.3%; Score 445.5; DB 4; Length 333;
 Best Local Similarity 30.3%; Pred. No. 4.5e-35; Matches 120; Conservative 30.3%; Mismatches 25; Indels 87; Gaps 9; Gaps -GNSHV 76

Db 62 NQPLINPLNIVGPE---MSNLTRNIRSLLGSGI-PSLDTVAKYVVSSEGKHLRPLMVL 116
 Qy 177 LASQRRAETEMIHAASLLHDVIDASERTRRNAPSGNQAFGNKMAILAGDFILGRASVA 236
 Db 4 NENVKPLDLSVELLAGMDRNRNALIREMRSRAPHPIPEVTALVAGGRKLRLPMLV 62
 Qy 117 MAQATEVAKVQGNWKRUVVEPVNVGLAPPVELNDKNPDMMNNRSGPLTKDGIEGOTNSI 176

Db 63 -----AAARLCGQ-----GNSHV 76
 Db 132 MADTSMQVMRLLANASATIAEGVLQL-----TAQDVSTTDTDVQIVRGKTA 181
 Qy 294 SLIAKSCRASALIGGATPEVADAYAAYGRNLGLAQFOIVDDMLDYTVATDGGPKPAGDLO 353
 Db 182 ALPSAATEAGVAGADPAVQQALFDYGDALGIAFQIVDDMLDYTVATDGGPKPAGDLO 241
 Qy 354 LGLATAPALFA-----WGHHAELGPMPKRFSDPGVERARLVEKGLEKTR 402
 Db 242 ERKLTLPVKIKARADEAERAFWER-----TIGQRODEADLATEILRRREALEAR 295
 Qy 403 ALABEYAKQKALDAIRTPESPARALEQITDKLIR 438
 Db 296 ADAIAWAGRAKKAALQAAPDQPPLRRLADLFVUSR 331

LENGTH: 333 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-803-951-29

Query Match Score 445.5; DB 4; Length 333;
 Best Local Similarity 30.3%; Pred. No. 4.5e-35;
 Matches 120; Conservative 64; Mismatches 125; Indels 87; Gaps 9;

Qy 62 NQPLINPLNLVGBE--MSNLTSNRLSLLGGCH-PSLDTVKYVYSEGHKIRPLMVL 116
 Db 4 NENVSKPLDRSLVTELAGMDRNALIRERMASRHPAPEVTALVEAGGRLRPMVL- 62

Qy 117 MAQATEVAPKVKVYEVPEVNEGLAPEVINDKNPDMNNNRSGPLTKDGTIEGQNSNI 176
 Db 63 ---AARLIGYQ----GNSHV 76

Qy 177 LASQRRLAEITEMTHAASLHDDVIDASETTRNAPSGNQAFGNKMAILAGDPFLGRASVA 236
 Db 77 L---LAIAVEFTIATLHDDVVDSSQRGRPTANLLWNKSSVLFVGDLFLARSFQL 131

Qy 237 LARLRNPVIELLATVIANLVCEFMQLKNTYDAEATATE--TDFYIQLTYLKTA 293
 Db 132 MADTESSQMRNLANASATIAESEVQL-----TAADQVSTTEDTYIQVRGKTA 181

Qy 294 SIAIAKSCASALIQLGATPEVADAYAVGRNLGAFOQIVDDMJDYTVSATDLKRPAGDLO 353
 Db 182 ALPSAAATPAGAVAGADPAVQQLDFYCDALGAFQIVDDLYGGSTTTTGKVNGDDFR 241

Qy 354 LGIATAPALFA-----WKGHHAELGPMTKRFKSDPGOVERAREBLVEKSDGLEKTR 402
 Db 242 ERKLTLPTKAARADEERERAWER-----TIGQGRDEADLATALEIIRRREALAAR 295

Qy 403 ALAEYAAOKALDAIRTPESPARKALEOILTGVLT 438
 Db 296 ADAIAWAGRKAALQAAQADQPLRRILLADLFVNSR 331

RESULT 4
 US-09-673-018-2
 Sequence 2, Application US/09673018
 Patent No. 6461642

GENERAL INFORMATION:
 APPLICANT: MATSUDA, Hideyuki
 APPLICANT: KAWAMURA, Makoto
 APPLICANT: YAJIMA, Kazuyoshi
 APPLICANT: IKENAKA, Yasuhiro
 APPLICANT: NISHI, Kenichi
 APPLICANT: HASEGAWA, Junzo
 APPLICANT: TAKAHASHI, Satomi
 TITLE OF INVENTION: METHOD FOR PREPARING COENZYME Q10
 FILE REFERENCE: 2000-1-372A/LC/00177
 CURRENT FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: JP 11/32657
 PRIOR FILING DATE: 1999-02-10
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 335
 TYPE: PRT
 ORGANISM: Agrobacterium sp.
 US-09-673-018-2

Query Match Score 439.5; DB 4; Length 335;
 Best Local Similarity 30.1%; Pred. No. 1.7e-34;
 Matches 115; Conservative 62; Mismatches 140; Indels 65; Gaps 5;

Qy 63 QPLINPL-NLVGPMSNLTSNRLSLLGGHPSLDTVKYVYSEGHKIRPLMVLMAQT 121
 Db 11 QASVKPLVLDTSPDMERVNQILSRAGSDVQMIPEVANHLISGGKRLRPMLTLASA--- 67

Qy 122 EVAPKVOGWEKVKVEPVNEGAPPEVINDKPNPDMNNMRSGPLTKDGEIEGOTSNILASQR 181
 Db 68 ---AMFGYEGDAHV --- 78

Qy 182 RLAETITEMIHASLLHDVIDASETTRNAPSGNQAFGNKMAILAGDPFLGRASVALRLR 241
 Db 79 KLIATSVEMHTPLHDDVVDESDLRKSTPARTIWIQNOASVLUVGDFLQAFRMNVDVG 138

Qy 242 NPEVILATVIANLVCEFMQLKNTYDAEATATE--TDFYIQLTYLKTA 301
 Db 139 SLDALDYLSTAASVIEGEVIOLS----VAKNMETTEDYLVIRAKTAALFAAAE 191

Qy 302 ASALLGGATPEVADAAYAVGRNLGLAQIVDDMLDVTVSATDLGKPAGADLQLGLATAPA 361
 Db 192 VGPVIAGTSKSDRNLKSYGNLGLAFOLVDDGGSASDLDKGNGDDREGKITLPV 251

Qy 362 LFAWKHAEELGPMTKRFKSDPGD----VERARELVEKSDSLXTRALAEYAOKALDAI 416
 Db 252 ILSYRRTGPEDRAFWREIAEGDSDSSDNLERALGLIKRYGGJSDTIARAQHYGTJARDAL 311

Qy 417 RTFPESSEPKALEQLTDKVLT 438
 Db 312 APLPVSEWWSALVEVIDFCIDR 333

RESULT 5
 US-09-117-609A-6
 Sequence 6, Application US/09217609A
 Patent No. 6071733

GENERAL INFORMATION:
 APPLICANT: MURAMATSU, Masayoshi
 APPLICANT: KOIKE, Ayumi
 APPLICANT: OGURA, Kyozo
 APPLICANT: KOYAMA, Tanetoshi
 APPLICANT: SHIMIZU, Naoto
 APPLICANT: CHO, Yenwei
 TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, NW - Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: US
 ZIP: 20036

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 SOFTWARE: WordPerfect 6.1 for Windows

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/217, 609A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/873, 235
 FILING DATE: 11-Jun-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: TOFFENETTI, Judith L.
 REGISTRATION NUMBER: 39, 048
 REFERENCE/DOCKET NUMBER: 10235/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-1776
 TELEFAX: 202-429-0796
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 320 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-217-609A-6

Query Match 18.6%; Score 409; DB 3; Length 320;
 Best Local Similarity 28.5%; Pred. No. 1.5e-31;
 Matches 106; Conservative 61; Mismatches 127; Indels 78; Gaps 6;

Qy US-08-873-235B-6

Db

Qy

Db

Db 61 AC-----GETN-LKH 69
 Qy 180 QRRLAETEMIHAASLLHDVVIDASETRRNAPSGNQAFGNKMAILACDFLGRASVALAR 239
 Db 70 AQKLAATEMLRATLVHDDVDESGURRGRTANAWNNQTAFLVGDFFLARAFLILVD 129
 Qy 240 LRNPVEILLATVIANLYVEGFMQLRKNTVDDIAEATATOETFDYLOKTYLTASLIAKS 299
 Db 130 LDNMILKDFSGTCEAEGEVQLQ---AQHQPDTE-DIYLOIINGKTSRLFELA 182
 Qy 300 CRASALIGCGATPEVADAYAAGRNLGLAFOQTVDLCKPAGADLQLQLATA 359
 Db 183 TEGAAILAG-KPEYREPLRFGEFGNAFQIDDLQYTSDDATLGKNGIDDLMEGKPTL 241
 Qy 360 PAFAMWK-HAEIGPMIKRKFSDPG-DVERARELYEKSDGELKTRALAEEYAQKALDAI 416
 Db 242 PIIAAMONTGEGDRLRRSIATGGTSSOLEQYTAIVNSGALDYCCHRATERALQAL 301
 Qy 417 RPPESPARAKEBQLTDKVLTR 438
 Db 302 EILPESTYRQALVNLTIALDR 323
 Qy 8 US-09-134-001C-3250
 ; Sequence 3250, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134, 001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3250
 ; LENGTH: 357
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3250

Query Match 15.8%; Score 346; DB 4; Length 357;
 Best Local Similarity 24.8%; Pred. No. 2, 4e-25;
 Matches 95; Conservative 73; Mismatches 147; Indels 68; Gaps 6;

Db 93 -----GSNNKPSDTRYV 105
 Qy 65 LINPLNL-VGPMSNLTSNIRSLGSGHPSLDTVAKYYVOSGKHIRPLMVLMAQATEVAPKVQWE 123
 Db 36 VINVAKINNINNEKVRERLEAISSQTLOPASFHLLSSGKRVPAFLSGQF--- 92
 Qy 124 AKPVQGEKVVYPVNEGLAPPEVINDKPNRSGPLTGEIGQTSNLASORRL 183
 Db 93 -----GSNNKPSDTRYV 105
 Qy 184 AETEMIHAASLLHDVVIDASETRRNAPSGNQAFGNKMAILAGDPLGRASVALARNP 243
 Db 106 AVALELHMATHVHDDVLDKSDKRGRLTISKWDQSTAILTGPNFLAMGLKHSEISDT 165
 Qy 244 EYIELLATVIANLYVEGFMQLKNTVDDIAEATATOETFDYLOKTYLTASLIAKS CRAS 303
 Db 166 RVIATISKSIIVDCRGELQFDQFN-----SNQITNYRIRNFKTALLIQSLTQVG 218
 Qy 304 ALLGGATPEVADAYAAGRNLGLAFOQIVDDMDYTVAATDLCKPAGADLQLGLATAPLF 363
 Db 219 ATSNASNDVIRKLKMGTHYGMSPQLIDDVLDFTSSEKKLGPKVGSDDLMNCHGHTLPVLL 278
 Qy 364 AWGHAAELGPMMKRFKSF-DPGDVERAEE-YQSKALDAIR 417
 Db 279 ENRKN---KTFKDQKISOLNPDSPQHAFETCTIROSSEIPOSQKISEKYLANKAINLID 334
 Qy 418 TFPESPARKALEQLTDKVLTRSR 440
 Db 335 ELEDGPNKELPFKLIKKGNSR NK 357

RESULT 9
 US-09-217-609A-2
 ; Sequence 2, Application US/09217609A
 ; Patent No. 601733
 ; GENERAL INFORMATION:
 ; APPLICANT: MURAMATSU, Masayoshi
 ; APPLICANT: KOIKE, Ayomi
 ; APPLICANT: OGURA, Kyozo
 ; APPLICANT: KOYAMA, Tanetoshi
 ; APPLICANT: SHIMIZU, Naoto
 ; APPLICANT: CHO, Yenwin
 ; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
 ; NUMER OF SEQUENCES: 29
 ; ADDRESSEE: Kenyon & Kenyon
 ; STREET: 1025 Connecticut Avenue, NW - Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: US
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 ; SOFTWARE: WordPerfect 6.1 for Windows
 ; CORRESPONDENCE ADDRESS:
 ; APPLICATION NUMBER: US/09/217, 609A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/873, 235
 ; FILING DATE: 11-Jun-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: TOFFENETTI, Judith L.
 ; REGISTRATION NUMBER: 39,048
 ; REFFERENCE/DOCKET NUMBER: 10235/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-1776
 ; TELEFAX: 202-429-0796
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 325 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-217-609A-2

Query Match 15.3%; Score 336.5; DB 3; Length 325;
 Best Local Similarity 26.7%; Pred. No. 1.7e-24;
 Matches 100; Conservative 59; Mismatches 148; Indels 67; Gaps 6;

Db 72 VGPMSNLTSNIRSLGSGHPSLDTVAKYYVOSGKHIRPLMVLMAQATEVAPKVQWE 131
 Qy 10 LNPYIIEVKRYECLQSDSETINKAHHLSSGGKVRPMFLVLSG----- 56
 Db 10 KVPVVPNEGILAPPEVINDKNPDMMNMRSGPLTKDGEIGEIGOTSNTIASQRRAEITEMIH 191
 Qy 57 -----FLNDTQKQDL-----IRTAVSLELVH 77

Query Match 15.3%; Score 336.5; DB 3; Length 325;
 Best Local Similarity 26.7%; Pred. No. 1.7e-24;
 Matches 100; Conservative 59; Mismatches 148; Indels 67; Gaps 6;

Db 78 MASLVDHDYDINSMDMERTNTSHIAFDKDTAIRTGHFLALARONIATINNSKFHOFISK 137
 Qy 252 VIANLYVEGFMQLKNTVDDAEATATOETFDYLOKTYLTASLIAKS CRAS ALIKA TP 311
 Db 138 TILEVCFGEFQDMADRFNYPISFTA-----YLRRINRKTAILEASCHIGALSSQDLE 190
 Qy 312 EVADAAYAAGRNLGLAFQIVDDMDYTTSATDLGKPGADDLQLGLATAPLFWKHAE- 370

Db 276 IH----RTAVILLECSVVGGILGGATEDEARIIRRARYCGLLFOVDDILDVTKSSE 329
 Qy 343 DKGPKAGADLQGLATAPALPAFKHAAELGPIMIKRKFSDFGIVERARELVEKSDGLEKTR 402
 Db 330 EIGKTAGKDLLTDKATYPKLM-----GLEKAK 356
 Qy 403 ALAEEYAQKALLDAIRTFESPARKALEQLTDKVLTR 438
 Db 357 EFAEELATRAKEELSSFDQIAAPLL-GLADYIAFR 391

RESULT 12
 Sequence 27; Application US/09187050B
 General Information:
 Applicant: Croteau, Rodney B
 Applicant: Hefner, Jerry
 Title of Invention: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
 File Reference: WSR12423
 Current Application Number: US/09/187,050B
 Number of SEQ ID NOS: 34
 Software: PatentIn Ver. 2.0
 SEQ ID NO 27
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Taxus canadensis
 CURRENT APPLICATION NUMBER: US/09/187,050B
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 27
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Taxus GGPP
 OTHER INFORMATION: synthase protein variant
 OTHER INFORMATION: variant
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1) .(393)
 OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
 OTHER INFORMATION: variant
 US-09-187-050-27

Query Match 12.8%; Score 280; DB 3; Length 393;
 Best Local Similarity 25.9%; Pred. No. 7,2e-19;
 Matches 118; Conservative 59; Mismatches 171; Indels 108; Gaps 15;

Db 23 TIRTAAPSRLRCLTPSRPSSWAAVSSASRVLVEDPDPNQLPLNVLGPEMSNLTSN 82
 Db 4 TAMAAGTOSLQRITVASQECMSMRSCP-----LTPPK---SFHGYNFN 45

Qy 83 IRSLLGS---GHPSLDTVAKYVYQSEGKHIRPLMVLMAQATEVAPKVQCMWEVVP 137
 Db 46 VPSSLAANCEIMCHLKLGSLSPLVKQCSVSSKSK-----TMAQLVDLAETEKAGKOTEDF 100

Qy 138 VNGLAPPEVLNDKPNRMNSGPLTKGE--EGTYSNLLSNSQRRI-----183
 Db 101 FNEYMKSKAVADAALD---KAITLEPEKTHESMRYSLLAGKRVTPALCIAACEBLVG 156

Qy 184 -----AEITEMTHAASLHDDV--IDASSTTRNAPSGNQAFGNKMTLAGDFLGLR 232
 Db 157 GSGLDAMPTACAMEIHMSLHDPLPMNDDFRRGPKTNKFVGEDTAVAGDAILSF 216

Qy 233 A---SVALAR----RNPEVIELATVIAN--LVEGEFMQLNKNTVDAEATATQTFD 282
 Db 217 AFBHIAVATSKVPSDRTLRLVSELGKTKTQSGLVGGQVVDITSEGAND-LKTLEWIH 275

Qy 283 YIQLQTKLTKTSAKSCRAUJGATPEVADAAYGRUGLAQFQVDDLDYTVSAT 342
 Db 276 IH----RTAVILLECSVVGGILGGATEDEARIIRRARYCGLLFOVDDILDVTKSSE 329

Qy 343 DKGPKAGADLQGLATAPALPAFKHAAELGPIMIKRKFSDFGIVERARELVEKSDGLEKTR 402
 Db 330 EIGKTAGKDLLTDKATYPKLM-----GLEKAK 356
 Qy 403 ALAEEYAQKALLDAIRTFESPARKALEQLTDKVLTR 438

RESULT 13
 Sequence 2, Application US/09187050B
 Patent No. 6043072
 General Information:
 Applicant: Croteau, Rodney B
 Applicant: Hefner, Jerry
 Title of Invention: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
 File Reference: WSR12423
 Current Application Number: US/09/187,050B
 Number of SEQ ID NOS: 34
 Software: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Taxus canadensis
 CURRENT APPLICATION NUMBER: US/09/187-050-2

Query Match 12.7%; Score 278; DB 3; Length 393;
 Best Local Similarity 28.9%; Pred. No. 1.1e-18;
 Matches 103; Conservative 47; Mismatches 127; Indels 80; Gaps 11;

Qy 117 MAQATEVAPKVOQWKEVVPNEGLAPIPEVNVNGLP:-----EGTSN 175
 Db 80 MAQLVDLAETEKAGDIEFDENEYMKSKAVADAALD---KAITLEPEKTHESMRYS 135

Qy 176 TIASORBL-----AEITEMTHAASLHDDV--IDASSTTRNAP 211
 Db 136 LIAGGKRVRPAlCIAACELVGSSDILAMPtACAMENITHMSLHDPLPCMNDDFERGKP 195

Qy 212 SGNQAFGNKMTLAGDFLGRA---SVALARL---RNPEVIELATVIAN--LVEGEF 261
 Db 196 TNHKVFGEDTAVAGDALSFAFEHTAVATSKVPSDRTLRLVISELGKTIQSGLVYGGQV 255

Qy 262 MOLNKTYDDATEATATQTFDYLQTKYLTAFLSIANSCRASALLGGATPEVADAAYAG 321
 Db 256 VDITSESDANV-LKTLEWIH----KTAVILLECSVVGGILGGATEDEARIIRRVA 308

Qy 322 RNLGLAFOIVDDMDLYTVSATDLGKPGAGDOLGLATAPALFAWKHHAELGPMIKRKFS 381
 Db 309 RCVGLIFQQVDDILDYTKSSEELGKPGKDLITDQATYPKLM-----350

Qy 382 PGDVERARELVKSQDGLEKTRALAEEYAKALDAIRTFESPARKALEQLTDKVLTR 438
 Db 351 -----GIEKAKEFAELATRAKEELSSFDQIKAAPLL-GLADYIAFR 391

RESULT 14
 Sequence 14, Application US/09187050B
 Patent No. 6043072
 General Information:
 Applicant: Croteau, Rodney B
 Applicant: Hefner, Jerry
 Title of Invention: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
 File Reference: WSR12423
 Current Application Number: US/09/187,050B
 Number of SEQ ID NOS: 34
 Software: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Taxus GGPP
 OTHER INFORMATION: synthase protein variant

Copyright GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 09:49:07 ; Search time 19 Seconds
 (without alignments)

460.345 Million cell updates/sec

Title: US-09-830-111A-2

Perfect score: 2194

Sequence: 1 MASPALRISSSSIASLR.....ESPPARKALEQLTDXVLTCSR 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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12: /cgcn2_6_ptodata/2/pubpaas/US60_NEWPUB.pep/*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	451.5	20.6	323	10 US-09-815-242-10321	Sequence 10321, A
2	451.5	20.6	323	10 US-09-815-242-13734	Sequence 13734, A
3	445.5	20.3	329	10 US-09-815-242-11142	Sequence 11142, A
4	440.5	18.5	322	10 US-09-815-242-12603	Sequence 12603, A
5	371.5	16.9	312	10 US-09-815-242-5315	Sequence 5315, AP
6	367.5	16.8	312	10 US-09-815-242-10573	Sequence 10573, A
7	347	15.8	326	9 US-09-738-626-4030	Sequence 4030, AP
8	340	15.5	350	9 US-09-925-637-66	Sequence 66, APPL
9	339	15.5	273	10 US-09-925-637-66	Sequence 66, APPL
10	302.5	13.8	307	10 US-09-815-242-11306	Sequence 11306, A
11	277	12.4	367	9 US-10-108-915-26	Sequence 26, APPL
12	260	11.9	299	10 US-09-815-242-10069	Sequence 10069, A
13	255	11.6	350	9 US-10-108-915-22	Sequence 22, APPL
14	254.5	11.6	232	9 US-10-108-915-14	Sequence 14, APPL
15	253	11.5	369	9 US-10-108-915-18	Sequence 18, APPL
16	252	11.5	377	10 US-19-934-778-2	Sequence 2, APPL
17	251.5	11.5	293	10 US-09-815-242-10630	Sequence 10630, A
18	247.5	11.3	316	9 US-10-108-915-45	Sequence 45, APPL
19	247	11.3	371	9 US-09-738-626-5880	Sequence 5880, APPL

ALIGNMENTS

```

RESULT 1
US-09-815-242-10321 ; Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELUTRA 011A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10321
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10321
Query Match Score 20.6%
Best Local Similarity 31.0%
Pred. No. 1.2e-30;
Length 323;
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Matches 116; Conservative 52; Mismatches 143; Indels 63; Gaps 4;

QY 71 LVGPEMSNLTSNRLSGSGHPSLDTVAKYVQSEGKIRPLMLMAQATEVAPKVQGW 130
Db 9 LTAQDMAGMVNAILEQNLSDVQINOLGYVITSGGGKIRPMIAVLAARAV-----GY 61

QY 131 EKVVEVPNEGLAPPEVLNDKNPDMNMNRSGPLTKDGBIEGOTSNTILASORRRAITEMI 190
Db 62 EGNAHVTI-----AALIEFI 76

QY 191 HAASLLHDVIDASETTRNAPSGNQAFGNKMAILAGDPLLGGRASVALARLRNPVEIELLA 250
Db 77 HTATLHDDVVDIDESMRKGATAAAFGNAAASVLYGVDFYTRAFQMMTSLGSLSLKVLVMS 136

QY 251 TVIANLVEGEFFMQLKNTVDAEATATOETFDYLQKYLTKRASILAKSCRASALLGGAT 310
Db 190 PEEKGLODYGRIGTAFQQLDDLDYNDGEFLGRKAVGDDNEGKPTPLHMHGTP 249

QY 371 LGPMIKRKSFDPG---VERARELVEKSDGLEKTRALAEEYAQAKAIDAIRFPESPARK 426
Db 250 EQQMTIRATEQNGNRHLLEPVLEMNACGSLEWTRORAEEDKAIALQVLPDTPWRE 309

QY 427 ALBQTDKVTRSR 440
Db 310 ALIGLAHTAVORDR 323

RESULT 2

US-09-815-242-13734

; Sequence 13734, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: Prokaryotes

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13734

TYPE: PRT

LENGTH: 323

ORGANISM: Salmonella typhi

US-09-815-242-13734

RESULT 3

US-09-815-242-11142

; Sequence 11142, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: Prokaryotes

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11142

TYPE: PRT

LENGTH: 329

ORGANISM: Haemophilus influenzae

US-09-815-242-11142

Query Match 20.6%; Score 451.5; DB 10; Length 323;
Best Local Similarity 30.7%; Pred. No. 1.2e-30;

Matches 119; Conservative 49; Mismatches 133; Indels 65; Gaps 6;

Qy 71 LVGPEMSNLTSNRLSLSGSGHSSLDVAKYYQSEGKHIRPLMVLMLMAQATEVAPKVQGW 130
 Db 15 LADPDMQKVNNQLLAQNSDPLIGOLGFYIQQGGKRIRPLJAVLAARSU----- 65

Qy 131 EKVVEVPVNIGLAPPVELNDKNDPDMNNRSGPLTKDGBIEGGOTSNILASQRRLABITEMI 190
 Db 66 -----GFEGLNSITCAT-----FVEFI 82

Qy 191 HAASLLHDVIDTASETRRNAPPNGNOFGNKWMAILAGDFLLGRASVALARLNPEVIELLA 250
 Db 83 HPSLLHDVVEDSDMERGRATANAEFGNAASVLVGDFIYTAFOLVALESKILSIMA 142

Qy 251 TIANLVEGEFMQLKNTVD-DIAEATATQETDYLOKTYLKTTASLIAKSCRASALIGGA 309
 Db 143 DATNVLAEGEVQQLMNNTDPEISEAN-----YMRVYISTSTARLFEVAGGAAAVAGG 194

Qy 310 TPEVADAYAYGRNLGLAQIYDDMLQDXTVSTDLGRPGADLQLGLATAPALFWAMRH-H 368
 Db 195 TEAQEKALODYGRYLGTAFQQLDDVLDYSANTQALGNVNGDDLAEGKPTPLPHMRHGN 54

Qy 369 AELGPMIKRKFSDFGDYVERARE--LVEKSDGILEKTRALAEFYAQKALDAIRTFPESPAR 425
 Db 255 AQAALIREAIEGGKRAEDDEVLAINTEHKSLDYAMNRRAKEAQAQDAFILEPSEYK 314

Qy 426 KALEQL 431
 Db 315 QALISL 320

RESULT 4

US-09-815-242-12031

Sequence 12031, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION

APPLICANT: Hasebeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELUTRA.011A

CURRENT APPLICATION NUMBER: US/09/815, 242

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269, 308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12031

LENGTH: 322

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-815-242-12031

RESULT 5

US-09-815-242-12603

Sequence 12603, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION

APPLICANT: Hasebeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELUTRA.011A

CURRENT APPLICATION NUMBER: US/09/815, 242

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269, 308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12603

LENGTH: 322

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-12603

Query Match Score 405; DB 10; Length 322;
 Best Local Similarity 29.8%; Pred. No. 9.8e-27;

Query Match Score 371.5; DB 10; Length 322;
 Best Local Similarity 16.9%; Pred. No. 6.6e-24;

Matches	101; Conservative	69; Mismatches	144; Indels	63; Gaps	5;
Matches	97; Conservative	68; Mismatches	142; Indels	59; Gaps	4;
Qy	6.9 LNLVGPPEMSNUTSNRLSLSGGHPSLDTVKV---YYVQSEGKHIRPLMVLWAQATEVA 124	7.5 EMSNLTSNIRSLSGHSGLDTVKVYYVQSEGKHIRPLMVLWAQATEVA PKVQGWKEKV 134	Qy	7.5 EMSNLTSNIRSLSGHSGLDTVKVYYVQSEGKHIRPLMVLWAQATEVA PKVQGWKEKV 134	Qy
Db	2 INVAKLNMMNNBKKYVEORLEKAIKSKDSVLEQASLHLSSGGKVRPAFVILSSQ---- 56	4 BIKVVEORLEKAIKSKDSVLEQASLHLSSGGKVRPAFVILSSQ---- 48	Db	4 BIKVVEORLEKAIKSKDSVLEQASLHLSSGGKVRPAFVILSSQ---- 48	Db
Qy	125 PKVQGWEKVVEVPVNEGLADPPEVLNDKNPDMNMRSGPLTKDGRIGQTSNILASQRLLA 184	135 EVPVNEGLAPPEVLNDKNPDMNMRSGPLTKDGRIGQTSNILASQRRAEITEMIHAS 194	Qy	135 EVPVNEGLAPPEVLNDKNPDMNMRSGPLTKDGRIGQTSNILASQRRAEITEMIHAS 194	Qy
Db	57 -----FSKDEQTSEQTQV-----A 71	49 -----FGKDEQTSEQTQV-----AVALELHMAT 73	Db	49 -----FGKDEQTSEQTQV-----AVALELHMAT 73	Db
Qy	185 EITEMIHAASSLHHDDVIDASETTRNAPSGNQAFGNKMAILAGDFLIGRASVALARLRNP 244	195 LLHDHDVIDASETTRNAPSGNQAFGNKMAILAGDFLIGRASVALARLRNPBEVILATVIA 254	Qy	195 LLHDHDVIDASETTRNAPSGNQAFGNKMAILAGDFLIGRASVALARLRNPBEVILATVIA 254	Qy
Db	7.2 VALELHMATLVHDDVIDKDKSRKGKLTISKWDQTTAILTGFLALGLEHLMAVKDNR 131	7.4 LVHDDVIDKDKSRKGKLTISKWDQTTAILTGFLALGLEHLMAVKVNVRHOLIESLV 133	Db	7.4 LVHDDVIDKDKSRKGKLTISKWDQTTAILTGFLALGLEHLMAVKVNVRHOLIESLV 133	Db
Qy	245 VIELLATVANLVEGPFMQLKNTVDAAIEATAQETFDYLQKTYLKTASLIAKSCRASA 304	255 NLVEGEFFMQLKNTVDAAIEATAQETFDYLQKYLKUSLIAKSCRASALLGGATPEVA 314	Qy	255 NLVEGEFFMQLKNTVDAAIEATAQETFDYLQKYLKUSLIAKSCRASALLGGATPEVA 314	Qy
Db	13.2 VHQLISESTVDCREBLFQDQFN-----SQQTINTYRRINRKTAQLIQUSTEVGA 184	13.4 DVCHGELFOPODQN-----SQQTINTYRRINRKTAQLIQUSTEVGAITSQSDKETV 186	Db	13.4 DVCHGELFOPODQN-----SQQTINTYRRINRKTAQLIQUSTEVGAITSQSDKETV 186	Db
Qy	305 LLGGATPTEPVDAAYAGRNLGLAQIIVDDMLDYTVSATDLGKPGAGDQQLGATAPALFA 364	315 DAAVYGRNLGLAQIIVDDMLDYTVSATDLGKPGAGDQQLGATAPALFAWKHAEGLPM 374	Qy	315 DAAVYGRNLGLAQIIVDDMLDYTVSATDLGKPGAGDQQLGATAPALFAWKHAEGLPM 374	Qy
Db	185 ITSQSDKETWRKLKMGHIGYIGMSQIIDDVLDFTSTEKKLGKPVGSDLNLGHITLPIILLE 244	187 RKLKGWIGHIGMSQIIDDVLDFTSTEKKLGKPVGSDLNLGHITLPIILLE KNDPKFLK 246	Db	187 RKLKGWIGHIGMSQIIDDVLDFTSTEKKLGKPVGSDLNLGHITLPIILLE KNDPKFLK 246	Db
Qy	365 WKHHABLGPMK- RKFSDGCDVERARELYEKSGLEKITAEEYAQKALDAIRTPES 422	375 IK- RKFSPGCDVERARELYEKSGLEKITALAEEYAQKALDAIRTPESPKALEQIT 432	Qy	375 IK- RKFSPGCDVERARELYEKSGLEKITALAEEYAQKALDAIRTPESPKALEQIT 432	Qy
Db	245 MRKQDPDFKLKIEQLRDRSEREFEBCIQIRKSIDSIDEAKAVSSKVLSKALDLISELPDG 304	247 IEOQARRDSEREFEBCIQIRKSIDSIDEAKAVSSKVLSKALDLISELPDGPKSLLSLT 306	Db	247 IEOQARRDSEREFEBCIQIRKSIDSIDEAKAVSSKVLSKALDLISELPDGPKSLLSLT 306	Db
Qy	423 PARKALEQLTDKVLTRES 439	433 DKVLTR 438	Qy	433 DKVLTR 438	Qy
Db	305 HPKSLLLSLTKKMGSR 321	307 KKMGSR 312	Db	307 KKMGSR 312	Db

RESUL16
US-09-815-242-5315

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5312
LENGTH: 312
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5315

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10573
LENGTH: 326
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-10573

Query Match 16.8%; Score 367.5; DB 10; Length 312;
Best Local Similarity 26.5%; Pred. No. 1.4e-23;

Query Match 15.8%; Score 347; DB 10; Length 312;
Best Local Similarity 27.8%; Pred. No. 7.9e-22;

Matches 108; Conservative 56; Mismatches 146; Indels 78; Gaps 9;

Qy 59 PDPNQPLINPLNIVGPENSNLTSNIRSLGSHPSLDTVAKYVQSECKHIRPLMVLIMA 118
 Db 9 PDIERSLTETCELTQTLHTRNEDIEE-----ALVTLLAR----SGCKLRLPAFFELFA 57

Qy 119 QATEVAPKVQGWEEKVVEPVNEGLAPPEVNLNDKPNPDMNMRRSPLTKDGEIBEQTSNLIA 178
 Db 58 QL-----GDEKEQEKQOLL 71

Qy 179 SQRRLAITEMTHAASLHHDDVIDASERTRNAPSNGQAFGNKMAILAGDFLLGRASVALA 238
 Db 72 --KIAASLEILLEMATLTHDDIIDSPLRGAVTIQSQIGRDAVYVGDLLTEFFFLIA 128

Qy 219 RLRN-PVEIELLATVIANULVEGFEMQLKNTVDAIEATAQTEDFYVQKTYLKKTASLIA 297
 Db 129 DAWNGSEPMKINACGMKRILLGELDQMSHRFRDRMSIPA-----YLRSVNCKTAELFS 181

Qy 298 KSCRASALLGGATPEVADAYAYGRNLGLAFQIVDDMDLYTYSATDICKPGAGDLQGLLA 357
 Db 182 LSCLLEGAFGHSSKEVORLAKRIGHIGAQFYQYDLDYTDATTETLKKPAELEDLSQGVY 241

Qy 358 TAPALFAWKHAELGPMLKRFKSPDG--DVERARE--LVKSDGLEKTRALAEYAQK 411
 Db 242 TLPLLFAY---QAPDVFSPLDKGRAITLLEAAEVALNDYHGTVEAQFAFKKVTK 297

Qy 412 ALDAIRTPESPARKALEQTLDKVLTRS 439
 Db 298 ATTDIQQLPFDGTAKETLSSLTEILHRS 325

RESULT 9
 US-09-925-637-66
 ; Sequence 66, Application US/0925637
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi,
 ; TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Polypeptides*
 ; FILE REFERENCE: PB860
 ; CURRENT APPLICATION NUMBER: US/09/925,637
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/23773
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US 60/151,933
 ; PRIOR FILING DATE: 1999-09-01
 ; PRIOR APPLICATION NUMBER: US 08/781,986
 ; PRIOR FILING DATE: 1997-01-03
 ; PRIOR APPLICATION NUMBER: US 08/956,171
 ; PRIOR FILING DATE: 1997-10-20
 ; PRIOR APPLICATION NUMBER: US 60/009,861
 ; PRIOR FILING DATE: 1996-01-06
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 66
 ; LENGTH: 273
 ; TYPE: PRT
 ; ORGANISM: *Homo sapiens*
 ; FEATURE:
 ; NAME/KEY: MISCELLANEOUS FEATURE
 ; LOCATION: (261)-(261)
 ; OTHER INFORMATION: Xaa equals any amino acid
 ; NAME/KEY: MISCELLANEOUS FEATURE
 ; LOCATION: (271)-(271)
 ; OTHER INFORMATION: Xaa equals any amino acid
 US-09-925-637-66

Query Match 15.5%; Score 340; DB 9; Length 350;
 Best Local Similarity 27.4%; Pred. No. 3.4e-21;
 Matches 115; Conservative 58; Mismatches 155; Indels 92; Gaps 14;

Qy 35 RCTPT-SRSPSSNAAAVSSASRLVEPDP-----NOPLINPLNVLGPEMSNLTSNIRSLI 87
 Db 5 RTYPTRSHLGLGKEGSTVGLGASQYEFQGDFELTARINDANVQEELLHTLS----- 54

Qy 88 GSCHPSLDTVAKYVQSEGKHIRPLMVLMAQATEVAPKVGMEKVVVPNEGLAPEV 147

Db 111 TINYLRINRKTALIQISTEVGAITSQSDFKETVRLKLMIGHYIGMSFOIDDVLFTS 170
Qy 340 SATDLGKPGADIQQLQGLATAPALFAWKHAEGLPPIK--RKPSDPGVERARELVEKSDG 397
Db 171 TEKKLGKVGSIDLNGHTIPILEMRKNPDFKLKIQOLRRSERKEFECIQIRKSDS 230
Qy 398 LEKTRALAEYYAQQKALDAIRTFPESPARAKALEQIITDKV 435
Db 231 IDEKAVSSKYLSKALNLSLEPDGHPRSLXLSLTKRM 268

RESULT 10
US-09-815-242-11306
; Sequence 11306, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELTRRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11306
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11306

Query Match 12.4%; Score 272; DB 9; Length 357;
Best Local Similarity 23.8%; Pred. No. 2e-15;
Matches 106; Conservative 59; Mismatches 152; Indels 128; Gaps 12;

Db 19 IRSVIRTASPL-----RURCTPSR-----PSSWA-----ANVSS 52
Db 1 MSAVNINTWPRPSFLINQATRSRSRSPFISHFHGVNKLPSPLSITVAKRPTLAVLT 60
Qy 53 ASRLYEPDPNQPLNPLNUGPEMSNLTSNRLSILGSGHP-SLDTVAKYYVOSSEGKIRP 111
Db 61 KEDTVTEERKPIFDPKNIVNSKASAVNKAIDDAVSREPORQTHEAMRYSLLAGGRVRP 120
Qy 112 IMLVJLMAQATEVAKVQGMEKVVEPVNEMGLAPPEVLAQDKNPIMNNRSGPLTKDGEIEG 171
Db 121 VLCV-----AACBLVGGEBATAMP----- 140

Qy 172 QTSNIALASQRRAITEMHASLHDV--IDSETRNASEGNOEGNKALLAGFL 229
Db 141 ------ACAIEMHTMSLJHDDLPCLMONDLRGKPNHKVFGEDAVLAGDAL 188

Qy 230 LGRA---SVALARLNPEVIELLATVIANLVEGFMLQINTVDATEATATOTBTFDYLO 286
Db 189 LAFERHIASTRASGRGPRIVRALSIGSEGLVAGQVNINSEGIA----DVDE 243

Qy 287 KTYL---KTAISLIAKSCRASALIGGATPEVADAYAVGRNGLAFOVDDMLDVTYSAT 342
Db 244 RLEFTHVHKTALEGAVLGAILGGTDVEECKRFARYVIGLUFOVQVDDILDVTKSQ 303

Qy 343 DLKGAGADLQGLATAPALFAWKHAEGLPPIK--RKPSDPGVERARELVEKSDGLKTR 402
Db 304 ELGKTAGKDVLADVKTYPKL----- 330

Qy 403 ALAERYAQKALDAIRTFPESPARAKA 427
Db 331 VFAAKLNKRDQDQVGF-DPVKA 353

RESULT 11
US-10-108-915-26
; Sequence 26, Application US/10108915
; Patent No. US200201177204A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Shen, Jennie
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
; FILE REFERENCE: BB1286 US NA
; CURRENT APPLICATION NUMBER: US/10/108,915
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 26
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Glycine max
US-10-108-915-26

Query Match 12.4%; Score 272; DB 9; Length 357;
Best Local Similarity 23.8%; Pred. No. 2e-15;
Matches 106; Conservative 59; Mismatches 152; Indels 128; Gaps 12;

Db 19 IRSVIRTASPL-----RURCTPSR-----PSSWA-----ANVSS 52
Db 1 MSAVNINTWPRPSFLINQATRSRSRSPFISHFHGVNKLPSPLSITVAKRPTLAVLT 60
Qy 53 ASRLYEPDPNQPLNPLNUGPEMSNLTSNRLSILGSGHP-SLDTVAKYYVOSSEGKIRP 111
Db 61 KEDTVTEERKPIFDPKNIVNSKASAVNKAIDDAVSREPORQTHEAMRYSLLAGGRVRP 120
Qy 112 IMLVJLMAQATEVAKVQGMEKVVEPVNEMGLAPPEVLAQDKNPIMNNRSGPLTKDGEIEG 171
Db 121 VLCV-----AACBLVGGEBATAMP----- 140

Qy 172 QTSNIALASQRRAITEMHASLHDV--IDSETRNASEGNOEGNKALLAGFL 229
Db 141 ------ACAIEMHTMSLJHDDLPCLMONDLRGKPNHKVFGEDAVLAGDAL 188

Qy 230 LGRA---SVALARLNPEVIELLATVIANLVEGFMLQINTVDATEATATOTBTFDYLO 286
Db 189 LAFERHIASTRASGRGPRIVRALSIGSEGLVAGQVNINSEGIA----DVDE 243

Qy 287 KTYL---KTAISLIAKSCRASALIGGATPEVADAYAVGRNGLAFOVDDMLDVTYSAT 342
Db 244 RLEFTHVHKTALEGAVLGAILGGTDVEECKRFARYVIGLUFOVQVDDILDVTKSQ 303

Qy 343 DLKGAGADLQGLATAPALFAWKHAEGLPPIK--RKPSDPGVERARELVEKSDGLKTR 402
Db 304 ELGKTAGKDVLADVKTYPKL----- 330

Qy 403 ALAERYAQKALDAIRTFPESPARAKA 427
Db 331 VFAAKLNKRDQDQVGF-DPVKA 353

RESULT 12
US-09-815-242-10069
; Sequence 10069, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,655
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 1410
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 10069
 LENGTH: 299
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-815-242-10069

Query Match 11.9%; Score 260; DB 10; Length 299;

Best Local Similarity 27.5%; Pred. No. 1..6-14;

Matches 114; Conservative 45; Mismatches 104; Indels 152; Gaps 19;

Qy 49 AVSSASRLVEPD...-NQPLINPNLVPEMSNTNSRSLIGSHPSSLDTVAKYYVSEG 1.06

Do 14 ANQALSRFTAPLFLQNTPVVE-----TMQYALIGG-----G 4

Qy 107 KHIRPLMVLMLMAQATEVAPKVGWKEKVVEPVYNEGLAPPEVNLNDKNPDMNNMRSGPLTKD 1.66

Do 45 KRDPFLV---PAT-----55

Db 117 GEIEGOTSNILASORRRAEITMTHAASLHDDY--IDASETRRNAPSGNQAFGNKMAIL 2.24

Db 56 GMFEGVSTNTLDAP---AAAVECTHAYSLIHDLPAMDDDRJRGPLTCVFGEBANAIL 1.12

Qy 225 AGDILLGRASVALARLRIPEV----TELL-----ATVIANLVGEFWQL---KNTVDD 2.70

Db 113 AGDALQTLAFLSISDADPMEVSQRDRISMELASGAGMCGQQLDAEGKHVPDL 1.72

Qy 271 AIEATAQETDYQLQTKTASLIASKCRASALLGG---ATPEVADAAYAGRNLG 3.25

Db 173 ALERIIRH---KTAGLIRAVRFLALSADKGKRALP-VLD--KYASIG 2.16

Qy 326 LAFOIVDDMLDYTVSATDQKGKAGDOLQGLATAPALPAWKHAEGLGPMIKRKFKPSDFGDV 3.85

Db 217 LAFOYQDDLDVYQGDATLGKROGADQOQKGKSTYAL-----LGLEQARK-----261

Qy 386 ERAREBLVERKSDSLGEKTRRAEAEAQKALDRAFTFESPARKALEQLTDVLRPSR 4.40

Db 262 -KARDLID--DARQSLKQLAEQ----SLDT-----SALEALADYIIQRNK 2.99

RESULT 13
 US-10-108-915-22

; Sequence 22, Application US/10108915

; Patent No. US2002017204A1

; GENERAL INFORMATION:

; APPLICANT: Cahoone, Rebecca E.

; APPLICANT: Shen, Jennie

; APPLICANT: Williams, Mark

; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases

; FILE REFERENCE: BBU286 USA NA

; CURRENT APPLICATION NUMBER: US/10/108-915

; CURRENT FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Microsoft Office 97

; SEQ ID NO: 14

; LENGTH: 232

; TYPE: PRT

APPLICANT: Cahoone, Rebecca E.
 APPLICANT: Shen, Jennie
 APPLICANT: Williams, Mark
 TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
 FILE REFERENCE: BBU286 USA NA
 CURRENT APPLICATION NUMBER: US/10/108-915
 CURRENT FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: Microsoft Office 97
 SEQ ID NO: 22
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Glycine max
 US-10-108-915-22

Query Match 11.6%; Score 255.5; DB 9; Length 350;
 Best Local Similarity 23.4%; Pred. No. 4..7e-14;
 Matches 59; Mismatches 141; Indels 107; Gaps 11;

Qy 37 TPTSRPSSWAAYSSAARSLYEPDPNQPLINPLNLYPEMSNLTSNIRSLIGSHP-SLD 95
 Db 33 TVTKRRAFSLSAVLT---VETEEKPKPFDKNTMDSVSLREPKIH 87

Qy 96 TVAKYYQSEGRHPRIVMLIMAQATEVAPKVGWERKVRPVLCV-----
 Db 88 BAMRYSLLAGGERVVRPVLCV-----ACFLVGGEHEATAMPA-----123

Qy 156 MMNRSGSPLTQDGIEGOTSNILASQRRAEITEMTHAASLHDDY--IDASETRRNAPSG 213
 Db 124 -----
 Qy 214 NOAFGNKMAILAGDFLIGRASVAL-ARLNPEVIELLATV-IANLVGEFMQLNTYDD 270
 Db 156 HTVFGEDVAVLAGDALLAFAFHIAASTRGASAPTRIAGELARSISSEGIVAGQVDI 215

Qy 271 AIEATAQETFYQYL-----KIASLIAKSCRASALLGGATPEVADAAYAGRNLG 3.26
 Db 216 NSEGLA---DVGLERLEFIVHVHTDAALLEGAVVGLAIGLGGTDEVEKLKFARYIGL 270

Qy 327 AFQIVDDMLDYTVSATDQKGKAGDOLQGLATAPALFAWKHAEGLGPMIKRKFKPSDFGDV 3.86
 Db 271 LFQVVDDILDVTKSQFLGKTAGDQJVAKVITYPKGL-----307

Qy 387 RARELVKSDGLEKTRALAAEYAQKALDARTFPESPARKA 4.27
 Db 308 -----GTEKSKEFAALKNDQDOLQAGF--DPVKAA 3.36

RESULT 14
 US-10-108-915-14

Sequence 14, Application US/10108915

; Sequence 14, Application US/10108915

; General Information:
 ; APPLICANT: Cahoone, Rebecca E.
 ; APPLICANT: Shen, Jennie
 ; APPLICANT: Williams, Mark
 ; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
 ; FILE REFERENCE: BBU286 USA NA
 ; CURRENT APPLICATION NUMBER: US/10/108-915
 ; CURRENT FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: Microsoft Office 97

; ORGANISM: *Oryza sativa*
us-10-108-915-14

Query Match 11.6%; Score 254.5; DB 9; Length 232;
Best Local Similarity 29.3%; Pred. No. 3.1e-14;
Matches 75; Conservative 39; Mismatches 93; Indels 49; Gaps 6;
QY 187 TEMIHAASLHLDDV--IDASERRNAPSGNQAFGNKMAILACDFLIGRASVALR----- 240
Db 1 TSLQHTMWSLVHDDLCMDPCMDNDLRLRGPKPHVYGEPIAVLTGDAALSLSFHMARFDSPY 60
QY 241 -----RNPEVELLAFTVIANLVEGERMLQKNTIVDIAEATRQEFDY-YLKTVIL-KT 292
Db 61 PRIDADRHPARVVRAGBLARTCISGLVAGQVD--LEMGTSTETVPLERLEYTHLHT 118
QY 293 ASLIAKSCCRASALLGGATPPEVADAAYAAGRNLGAFOQIVDDMLDYVSATDGKPGADL 352
Db 119 AMLLEASVIGILGGSDEQTESLRMARSIGLFLQWDDLDVTSSERLGKAGDL 178
QY 353 QLGLATAPALFAWKHHABLGPMKRKPSDPGVERARELVEKSDGLEKTRALAEVAQKA 412
Db 179 ASDKTTVPKL-----GLEKSREFAEKULSDA 205
QY 413 LDATRTPESPARKAL 428
Db 206 REQLSGFDOETAPELL 221

RESULT 15

US-10-108-915-18

; Sequence 18, Application US/10108915

; Patent No. US20020177204A1

; GENERAL INFORMATION:

; APPLICANT: Cartoon, Rebecca E.

; APPLICANT: Shen, Jennie

; APPLICANT: Williams, Mark

; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases

; FILE REFERENCE: BB1286 US NA

; CURRENT APPLICATION NUMBER: US/10/108,915

; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238

; PRIORITY FILING DATE: EARLIER FILING DATE: 1998-12-01

; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592

; PRIORITY FILING DATE: EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Microsoft Office 97

; SEQ ID NO: 18

; LENGTH: 369

; TYPE: PRT

; ORGANISM: Glycine max

US-10-108-915-18

Query Match 11.5%; Score 253; DB 9; Length 369;
Best Local Similarity 25.2%; Pred. No. 9.3e-14;
Matches 105; Conservative 54; Mismatches 163; Indels 94; Gaps 11;

QY 59 PDPNPQPLINPLNPGPEMSNLTSNIRSLGSHPSL-----DTVAKYVQDS 104
Db 10 PRPTSMINTPSHLLPPFHFTLUTTLKLASGTPKLSSFLPVASVPTKEHHTVTOEIQ- 68
QY 105 EGKHIRPLVLMLMAQATEVAKVQGVWPEKVVEPVNEGLAPPENLNDKNPDMNMNRSGPLT 164
Db 69 -----LQDTPLNFDPKGYMTAKAHITVNQALDAATLRLPHKIHOMARYSLA 115
Qy 165 KDG-----EIGQTSNLLASORRLABITEMIHAASLHLDDV--IDASERRNAP 211
Db 116 GGKRVRPVLCIACELVGSTE--ATAPAACAVEMHTMSLJHDLCMDNDLRLRGPK 172
QY 212 SGNQAFGNKMAILAGDELIGRA-----SVALARLNPEVELLATVIA-NJUJGEFM 262
Db 173 TNHKVYGEDDVALLAGDALLAFAPEHVAESTCYSPSRVRAIGELAKSIGREGVQVV 232
QY 263 QLKNTVDDATEATAQETFDYVLOQKTYLKTAISLIAKSCRASALLGGATPEVADAAYGR 322

Db 233 D---IDSEGIVANYGLETELEFI--HVHTTALEAVLGLAVGGSDEEVEKLKFAR 285
QY 323 NGLAPOIQVUDMDLYTVSATDGLKPGADOLQGLATAPALFANKHHABLGPMIKRKFSDP 382
Db 286 CIGLFRQVDDIDVTKSSEELGFTAGKDVLADKVTFKL----- 326
QY 383 GDVERARELVEKSICLEKRALREYAQKALDARTFESPARKALECOLTPDKVLT 438
Db 327 -----GIDSKFEAOELLKDAEQOLSGF-DPPKAAPLFAINTYAYR 367

Search completed: January 16, 2003, 09:56:38
Job time : 21 secs

Copyright (c) 1993 - 2003 Compugen Ltd.	Gencore version 5.1.3						
OM protein - protein search, using sw mode							
Run on:	January 16, 2003, 09:42:36 ; Search time 38 Seconds (without alignments) 1113.135 Million cell updates/sec						
Title:	US-09-830-111A-2						
Percent score:	21.94						
Sequence:	1 MASPALRIRSSRSSIASLRL.....ESPARKALEQLTDDKVLTRSR 440						
Scoring table:	BLOSUM62						
Gapopen:	10.0 , Gapext 0.5						
Searched:	283224 seqs, 96134422 residues						
Total number of hits satisfying chosen parameters:	283224						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
Database :	PIR-73; * 1: Piri; * 2: Pir2; * 3: Pir3; * 4: Pir4; *						
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
1	1023	46.6	473	1	XUBYTP		trans-pentaprenyl di-trans,poly-cis-trans pentaprenyl geranylgeranyl pyrophosphate synthetase; probable trans-pre solaneryl diphosphoryl transferase protein C24A11.9 [hypothetical prote prenyl transferase probable trans-pre octaprenyl-diphosph octaprenyl diphosph octaprenyl diphosph octaprenyl-diphosph octaprenyl synthet octaprenyl diphosph geranyltransferase octaprenyl-diphosph octaprenyl diphosph octaprenyl diphosph octaprenyl diphosph octaprenyl synthet polyprenyl synthet heptaprenyl diphosph octaprenyl-diphosph probable heptaprenyl diphosph octaprenyl-diphosph octaprenyl-diphosph octaprenyl-diphosph octaprenyl-diphosph
2	910.5	41.5	378	2	JC5429		
3	823.5	37.5	356	2	T43193		
4	676.5	30.8	323	2	A40433		
5	664.5	30.3	323	2	T06874		
6	664.5	30.3	323	2	AH1818		
7	661.5	30.2	323	2	S73189		
8	604.5	27.6	323	2	G87775		
9	602.5	27.5	277	2	F96813		
10	583.5	26.6	390	2	C86306		
11	574.5	26.2	379	2	A84759		
12	561	25.6	297	2	AB5109		
13	451.5	20.6	323	2	B91137		
14	451.5	20.5	323	2	E85982		
15	451.5	20.6	323	2	AD2654		
16	451.5	20.6	323	2	AD0903		
17	445.5	20.3	329	2	I64160		
18	424.5	19.3	348	2	AB2322		
19	420.5	19.2	362	2	AB3443		
20	418.5	19.1	323	2	AB0427		
21	418.5	19.1	338	2	AD2654		
22	418.5	19.1	358	2	H74435		
23	415	18.9	338	2	H87510		
24	411.5	18.8	320	2	B75457		
25	406	18.5	348	2	B6630		
26	405	18.5	322	2	C83075		
27	402.5	18.3	335	2	E070549		
28	395	18.0	336	2	A82688		
29	378	17.2	324	2	A81213		

Db 4 RSGAHHIKLSSRRCRFKSSFAVLAVALNASKLVTPI---KILWNPNPLSLVSKEMNTLAKN 59
QY 83 IRSLLGSGHPSLDTVAKYVQSBGKHIRPLMVLMAQATEVAPKVQ----GWEKNEV 136
Db 60 IVALIGSGHPVNLKVTSYFETEGKQRPLVLUMLSLALSEIPMTNRNLKIDKSVPEP 119
QY 137 PV-----NEGLAPPVBLNDKNPDMMNMRSGPLTKDGETEGQTSNILASORRL 183
Db 120 PIYSKPSONQLFORPAssISPLHLHGTP-LNPLTKCPEPLPETFDKQGILPKRQL 178
QY 184 AEITTEMHAASLHDVDASETTRNAPSGNQAFGNMKAIIAGDFLIGRASVALARLRNP 243
Db 179 AEIVEMIHTASLHDVDAHSDFTRGRPSGNAAFTNKMAVLAGDFLIGRATVSI RLHNP 238
QY 244 EVELLATVIANLVEGERMQLNTVDIAEATATQTFDYLQKTYLTASLIAASCRAALL 275
Db 239 EVELMSNISIANLVEGERMQLNTSIDADITIENGKLLPVPSKKLEVKBHDERRVPSRQ 298
QY 276 -----ATOBTFDYLQKTYLTASLIAASCRAALLDVTQGKPGAGDOLGLATAAPLAWK 326
Db 299 QGLQLSHQIETIAFEYIHKYTLKTAALISKSCRCRAILSGASPAVIDECYDFGRNLGI 358
QY 327 AFOIVDDMLDYVSATDGKPGAGDOLGLATAAPLAWKHAELGMKIKFSGDGV 386
Db 359 CFQLVDDMDLDFTVSGKLPKGPSGADLKLGIAATPVLPAWKEDPSLGPLISRNFSERGDVE 418
QY 387 RARLVEKSDGLEKTRALAEVHQKALDAIRTPESPARKALEQTDKVLTCSR 440
Db 419 KTIDSVRUHLNGIAKTKLIAEVTRDQLAKQNLRSPLSNDARSLFLUNSLITRK 473

RESULT 2

JCS5429 di-trans,poly-cis-decaprenylcistransferase (EC 2.5.1.31) [similarity] - fission yeast (S. pombe)

N:Alternate names: decaprenyl diphosphate synthase
C:Species: Schizosaccharomyces pombe
C:Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 28-Jul-2000
C:Accession: JCS5429; T50407
R:Suzuki, K.; Okada, K.; Kamiya, Y.; Zhu, X.F.; Nakagawa, T.; Kawamukai, M.; Matsuda, H.
J:Biochem. 121, 496-505, 1997
A:Title: Analysis of the decaprenyl diphosphate synthase (dps) gene in fission yeast sug
A:Reference number: JCS5429; MUID:9729041; PMID:9133618
A:Accession: JCZ429
A:Molecule type: DNA
A:Cross-references: DDBJ:D84311; NID:91845554; PIDN:BAA12314.1; PID:91845555
R:McDougall, R.C.; Rojandram, M.A.; Barrell, B.G.; Saunders, D.; Harris, D.
Submitted to the EMBL Data Library, January 2000
A:Reference number: 225059
A:Accession: T50407
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <Suz>
A:Cross-references: EMBL:D89265; NID:91749737; PIDN:BAA13926.1; PID:91749738
A:Cross-references: Strain PR45
A:Experimental source: strain PR45
C:Superfamily: prenyl transferase A

Query Match 37.5%; Score 823.5; DB 2; Length 356;
Best Local Similarity 50.0%; Pred. No. 5_se-50;
Matches 175; Conservative 56; Mismatches 92; Indels 27; Gaps 4;

Db 67 NPLNLUVGPMNSLNLSNLSLGSCHPSLDTVAKYVQSBGKHIRPLMVLMAQATEVAPK 126
Db 32 NASHLJNKELEQSPGIROMLNSNSEFCLBECKYTTAQGKMRPSLVLUMSKATS--- 88
QY 127 VQGMKEVWVPPNNEGLAPPEVLUKNPDMMNMRSGPLTKDGETEGQTSNILASORRLAI 186
Db 89 FNGIDR-----SVDQKYTDDARS-----FSTGOILHSOLRAOI 125
QY 187 TEMIHAASLHDVDASETTRNAPSGNQAFGNMKAIIAGDFLIGRASVALARLRNP 246
Db 126 TEMIHAASLHDVDAHSDFTRGRPSGNAAFTNKMAVLAGDFLIGRATVSI RLHNP 185
C:Genetics:

A:Gene: dps; SPDB:SPBPJ69.01; SPDB:SPBPJ694.01
A:Map Position: 2L
A:Introns: 325/3
C:Supersfamily: prenyl transferase A
C:Keywords: transferase

Query Match 41.5%; Score 910.5; DB 2; length 378;
Best Local Similarity 51.1%; Pred. No. 5_1e-56; Mismatches 60; Indels 27; Gaps 3;

QY 67 NPLNLUVGPMNSLNLSNLSLGSCHPSLDTVAKYVQSBGKHIRPLMVLMAQATEVAPK 126
Db 32 NASHLJNKELEQSPGIROMLNSNSEFCLBECKYTTAQGKMRPSLVLUMSKATS--- 91
QY 127 VQGMKEVWVPPNNEGLAPPEVLUKNPDMMNMRSGPLTKDGETEGQTSNILASORRLAI 186

Db 92 ID-----RSVgdkyvddrs-----FSTGQILSQRQAQI 125
QY 187 TEMIHAASLHDVDASETTRNAPSGNQAFGNMKAIIAGDFLIGRASVALARLRNP 246
Db 126 TEMIHAASLHDVDAHSDFTRGRPSGNAAFTNKMAVLAGDFLIGRATVSI RLHNP 185
Db 186 ELLATVIANLVEGERMQLNTVDIAEATATQTFDYLQKTYLTASLIAASCRAALL 306
Db 186 ELLATVIANLVEGERMQLNTVDIAEATATQTFDYLQKTYLTASLIAASCRAALL 306
Db 186 ELLATVIANLVEGERMQLNTVDIAEATATQTFDYLQKTYLTASLIAASCRAALL 306
Db 186 ELLATVIANLVEGERMQLNTVDIAEATATQTFDYLQKTYLTASLIAASCRAALL 306
QY 367 HHAELGPMKIKFSDPGVERABLVEKSDGLEKTRALAEVHQKALDAI 416
Db 305 KYPELGAMIVNRHMPSD1QRARSIVECSDATEQPIWTIAEVYIKKRPSSV 354

RESULT 4

S76966

Geranylgeranyl pyrophosphate synthase crtE homolog - *Synechocystis* sp. (strain PCC 6803)
 N; Alternate names: hypothetical protein_sir0611
 C; Species: *Synechocystis* sp.
 A; Variety: PCC 6803
 C; Accession: S79666; S74427
 C; Date: 14-Feb-1997 #text_change 25-Apr-1997 #text_change 21-Jul-2000
 A; Cross-references: EMBL:D90917; GB:AB001339; PID:gi1653836; PMID:g342616
 A; Cross-references: EMBL:D90917; GB:AB001339; PID:gi1653836; PMID:g342616
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 A; Accession: S74427
 A; Cross-references: EMBL:D90917; GB:AB001339; PID:gi1653836; PMID:g342616
 A; Cross-references: EMBL:D90899; GB:AB001339; PID:gi1651650; PMID:g165165
 A; Residues: 68-323 <KAW>
 A; Cross-references: EMBL:D90899; GB:AB001339; PID:gi1651650; PMID:g165165
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C; Genetics:
 A; Gene: crtE
 C; Superfamily: prenyl transferase A
 Query Match 30.8%; Score 676.5; DB 2; Length 323;
 Best Local Similarity 40.6%; Pred. NO. 8.7e-40;
 Matches 153; Conservative 63; Mis matches 102; Indels 59; Gaps 4;
 Query 65 LINPLNLVGP--EMSNLTNSNIRSLLGSSGHPSLDTVAKYVQVSEKGKHTRPLMVLLMAQT 121
 Db 1 MISTTSFLFAPVQDQLRLITDNLKLRLVGARHPILGAAAELFEEAGKVRPAIVLVSRAT 60
 Query 122 EVAPKVQGWKEVKVVEPVNEGLAPEVINDKPNPMMNMRSGPLTRKDGETGQTSNLSQR 181
 Db 61 -----LLDQ-----ELTARRH 71
 Query 182 RLAETTEMIHAASLLHHDDVIDASETRRNAPSNGNQAFGNMMAILAGDFFLGRASPALAR 241
 Db 72 RLAETTEMIHTASSLVHDVVDEADLRRNAPVNTNSLFDNRRAVLAGDFLFPAQSSWYLAND 131
 Query 242 NPEVIELLATVANLVLGECEFMQLKNTVDDAIEATAQETFDYLQKTYKTTASLIAKSCR 301
 Db 132 NLEVVKLILSEVLRDAESEBILQSINRFD-----TDITLEYLEKSYKFTASLIANSK 184
 Query 302 ASALLGGATPEVADAAYAYGRNIFGLAFOVQDDMLDYTVSATDQGKPGAGDLQLGLHATAPA 361
 Db 185 AAAGVLSLSDARDVCDHLVEYKGHLGLAQFQVDDIDFTSSTEVLKXPAGGLISGNITAPA 244
 Query 362 LFAWKHHAELGPIMIKRKFSPDPGDVERARELYEVKSDGLEKTRALAEYQQAKDALAIRTFPE 421
 Db 245 LFAMEKYLPIGLKLIEREPAQGDLQLEAQELVFGDGRIRSRELAANQALQARHLSVLEM 304
 Query 422 SPARKALEQLTDKVLT 438
 Db 305 SAPRESLLEVDYVGLR 321
 RESULT 5
 A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - *Cyanophora paradoxa*
 C; Species: *Cyanophora paradoxa*
 C; Accession: A40433
 R; Michalowski, C.B.; Loeffelhardt, W.; Bohnert, H.J.
 J. Biol. Chem. 26, 11866-11870, 1991
 A; Title: An ORF323 with homology to crtE, specifying prephytoene pyrophosphate dehydroge
 A; Reference number: A40433; MUID:91268060; PMID:1711042
 A; Accession: A40433
 A; Status: Preliminary

Db 370 M 370 :

J. Bacteriol. 171, 5222-5225, 1989
 A;Title: Cloning and sequencing of an Escherichia coli gene, nlp, highly homologous to tRNA^{Asp}
 A;Reference number: JV0027; MUID:89359178; PMID:2670911
 A;Accession: PV0010
 A;Molecule type: DNA
 A;Residues: 'T', 156-157, 196-323 <CHO>
 A;Cross-references: GB:X8873; NID:942128; PIDN:CAA48735.1; PID:9188220
 A;Gene: ispB
 A;Map position: 69 min
 C;Superfamily: prenyl transferase A
 C;Keywords: transferase

Query Match 20.6%; Score 451.5; DB 2; Length 323;
 Best Local Similarity 31.0%; Pred. No. 4.4e-24;
 Matches 116; Conservative 52; Mismatches 143; Indels 63; Gaps 4;

Qy	Db	Sequence	Start	End
QY	71	LVPGENMSNLTSNIRSLLGGSHPSDLTVAKYVQSEGKIRPLMLMAQATEVAPKVQGM	130	
QY	9	LTAQDMAGVMVAILEQLNQNSDQVLINQLGYYIVGGKIRPMTAVLARAVALA-----GY	61	
QY	131	ERVVEVPVNGLGAPPEVNLNDKNPDMMNRSGPLTKDGTEGOTSNILASQRRLAETTEMI	190	
QY	62	EGNAHVTI-----AALIEPI	76	
QY	191	HAASLHDYDVIDASERTTRNPAPSGMQAFGSKMIALGDTFLGRASVALARLNPPEVILLA	250	
QY	77	HTATLLHDYDIDESMRGRKATANAFGNASAVLGVDFITYTRAFFOMTISLGSIKLVLEMS	136	
QY	251	TVINIUVEGFMQLKNTVDDIAEATATQETFDYLQKLTKTSLIAKSCRSALGGAT	310	
Db	137	EAVNVIAAEGSYVTLQLMNNVNPDPD-----TEENYMRVYISKARLFEEAAACSGQLAGCT	189	
QY	311	PEVADAAVAYGRNIGLAFQTVDDMDLYTVSATDLGKPGAGAQOLQGLATAAPALFAWKHAE	370	
Db	190	PBEKGQLQDYGRYLSTAFOQDLDDLYWDGEQLGNVGDLDNEGKPTPLHMHGTP	249	
QY	371	LGPMIIRKFSDPGD----VERARASILVERKSDEGLKTRALAEYAKQAKDAIRTFPESPARK	426	
Db	250	EQAQMIRTAIBQNGNRHLLEPVLEAMNACGSLEWTRORAEEDKAIAALQVLPDTPWRE	309	
QY	427	ALEQTDKVIITRSR	440	
Db	310	ALIGLAHHIAVQRDR	323	

RESULT 14

B91137 octaprenyl diphosphate synthase [imported] - Escherichia coli (strain O157:H7, substrain O157:H7) 14

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C;Accession: B91137

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome comparison with O157:H7 strains

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B91137

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-23 <RAY>

A;Cross-references: GB:RA000007; PIDN:BAB7489_1; PID:gi1363539; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

A;Genetics:

C;Gene: EC4066

C;Superfamily: prenyl transferase A

Query Match 20.6%; Score 451.5; DB 2; Length 323;
 Best Local Similarity 30.1%; Pred. No. 4.4e-24;
 Matches 116; Conservative 51; Mismatches 132; Indels 87; Gaps 5;

Qy	Db	Sequence	Start	End
QY	71	LVGPENMSNLTSNIRSLLGGSHPSDLTVAKYVQSEGKIRPLMLMAQATEVAPKVQGM	130	

Db 9 LTAQDMAGYNAALEQLNSDLVQLINQLGYIIVSGGKRRIRPPIAVLALARV-----GY 61
 Qy 131 EKVVEVPNEGLAPEVINDKNPDMMNNRSGPLTKDGELEGTSNILLASQRRLAITEMI 190
 Db 62 EGNAHVTI -----
 Db 191 HAASLLHDDVIDASBTRNAPSGNQAFGNKMATLAGDFLGGRASVALARLRNPBEIELLA 250
 C;Accession: E85982
 Db 77 HTATLHDDVIDESDMRKGKATANAAFGNAASLVGDFITYRAFQMTSLSLKLEVMS 136
 Qy 251 T'VIANLVEGEFMOLKNTYVDAIEATATQETFDYLYLQKTYLTASLIAKSCRASALGGAT 310
 Db 137 EAVNIAEGEVLQLMNVNBDI -----
 Db 190 PEPEEKGLODYGRVLGTAFLQIDDLDDYNADGEQIGKNGVDDLNEGKPKTLPLHAMHH-- 246
 Qy 371 LGPMIKRKPSDPGDVERARELVEKSDG -----
 Db 247 -----
 Qy 415 AIRTFPESPARKALEQLDVKVLTCSR 440
 Db 298 ALQVLPDTPWREALIGLAHIAVQRDR 323

RESULT 15

E85982 octoprenyl diphosphate synthase [imported] - Escherichia coli (strain O157:H7, substrate C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: E85982
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, I.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimambanta, E.; Potamoussi, K.; Apodaca, NATURE 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; PMID:21074935; PMID:11206551
 A;Accession: E85982
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-323 <STO>
 A;Cross-references: GB:AE005174; NID:gi12517802; PIDN:AAG58321.1; GSFPDB:GN00145; UWGP:245
 A;Experimental source: strain O157:H7, substrate EDL933
 C;Genetics:
 A;Gene: 1spB
 C;Superfamily: prenyl transferase A

Query Match Score 20.6%; Score 451.5; DB 2; Length 323;
 Best Local Similarity 30.1%; Pred. No. 4..4e-24; Mismatches 51; Indels 87; Gaps 5;

Matches 116; Conservative 51; Mismatches 132; Indels 87; Gaps 5;

Db 9 LVGPPEMSNLTSIRSLGSGHPSLDTVAKYYVQSEGKHIRPLMVLLMAQATEVAPKYGW 130
 Qy 71 130
 Db 9 LTAQDMAGYNAALEQLNSDLVQLINQLGYIIVSGGKRRIRPPIAVLALARV-----GY 61
 Qy 131 EKVVEVPNEGLAPEVINDKNPDMMNNRSGPLTKDGELEGTSNILLASQRRLAITEMI 190
 Db 62 EGNAHVTI -----
 Db 191 HAASLLHDDVIDASBTRNAPSGNQAFGNKMATLAGDFLGGRASVALARLRNPBEIELLA 250
 C;Accession: E85982
 Db 77 HTATLHDDVIDESDMRKGKATANAAFGNAASLVGDFITYRAFQMTSLSLKLEVMS 136
 Qy 251 T'VIANLVEGEFMOLKNTYVDAIEATATQETFDYLYLQKTYLTASLIAKSCRASALGGAT 310
 Db 137 EAVNIAEGEVLQLMNVNBDI -----
 Db 190 PEPEEKGLODYGRVLGTAFLQIDDLDDYNADGEQIGKNGVDDLNEGKPKTLPLHAMHH-- 246
 Qy 371 LGPMIKRKPSDPGDVERARELVEKSDG -----
 C;LEKTRALABEYAQKALD 414

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Oy	367	HRAELGPMIKRKFSDFPVERARELVEKSDGIEKTRALAEEYAQKALDAIRTPESPARK	426	Qy	122	EVAPKVQGWKRVEPVNEGLAPPVELDNPDMNNMRSGPLTKGEIEEGOTSNTIASSQR	181
Db	305	KPELGAMIVNFNHPSDIQRARSLECTDAEQITIWAKETIKKARDLILQLPDSPARK	364	Db	61	-----LLDQ-----	ELTARH 71
Qy	427	AFLQLTDKVLTCSR	440	Qy	182	RRAEITTEMTHAASLILHDVIDDASETRNAPSNGNOAFGNKMAILAGDPLGRASVALRLR	241
Db	365	AFLFADAKVLTCSR	378	Db	72	RRAEITTEMTHAASLILHDVIDDASETRNAPSNGNOAFGNKMAILAGDPLGRASVALRLR	131
RESULT 3							
PREA_SVNY3				Qy	242	NPEVIBILATVIANLVEGFMLQKNTVDALEATATOETFDYIQLQTKYLKTPASLIAKSCR	301
ID	PREA_SVNY3	STANDARD;	PRT;	Db	132	NLEVVKLSEVIRDFAEGELQSINRFD-----TDTDILETYERSFKTASLIANSK	184
AC	P72580; P74758; 008042;	Created)		Qy	302	ASALLGCAPEVAADAYAAGRNLGLAFOIVDDMMDVTVSATDLGKGADLQLGLATA	361
DT	16-OCT-2001 (Rel. 40,	Last sequence update)		Db	185	AAGVLSDAPRDVCDHLYEYGRHLGLAFOIVDDMMDVTSPEVLGPAGSDLSGNITPA	244
DT	16-OCT-2001 (Rel. 40,	Last annotation update)		Qy	362	LFWAKWHAELGEMIKRKFSDFPGCDVERARELYEKSDGLEKTRALAEFYAAQKALDAIRTFPE	421
DE	Prenyl transferase (EC 2.5.1.-).			Db	245	LFAIMEKYPLIGKLIEREFAQAQDGLBQALELVEQGDGIRRSRELAANQALARQHUSVLEM	304
OS	Synechocystis sp. (strain PCC 6803).			Qy	422	SPARKALEQLTDKVLTTR	438
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.			Db	305	SAPRESLLEVLDVYLGSR	321
OX	NCBI_TAXID=1148;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEBLINE-96127529; PubMed=8590279;						
RA	Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,						
RA	Sugiyama M., Tabata S.;						
RA	"Sequence analysis of the unicellular cyanobacterium						
RT	Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb						
RT	region from map positions 64% to 92% of the genome.";						
RL	DNA Res. 2:153-166(1995).						
RN	[12]						
RP	SEQUENCE FROM N.A.						
RX	MEBLINE-97061201; PubMed=8305231;						
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,						
RA	Miyajima N., Hirokawa M., Sugiyama M., Sasamoto S., Kimura T.,						
RA	Soumochi T., Matsumoto A., Muraki N., Naruo K., Okumura S.,						
RA	Shimpo S., Takeuchi C., Wada T., Watanaabe A., Yamada M., Yasuda M.,						
RA	Tabata S.;						
RT	"Sequence analysis of the genome of the unicellular cyanobacterium						
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the						
RT	entire genome and assignment of potential protein coding regions.";						
RL	DNA Res. 3:109-136(1996).						
CC	-!- FUNCTION: POSSIBLE ROLE IN SYNTHESIS OF THE NONAPRENYL SIDE CHAIN						
CC	OF PLASTOQUINONE OR IN SYNTHESIS OF OTHER PRENYL CHAINS SUCH AS						
CC	UNDEPENRAYL PYROPHOSPHATE.						
CC	-!- SIMILARITY: BELONGS TO THE FPP/GCPP SYNTHETASES FAMILY.						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration						
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -						
CC	the European Bioinformatics Institute. There are no restrictions on its						
CC	use by non-profit institutions as long as its content is in no way						
CC	modified and this statement is not removed. Usage by and for commercial						
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/						
CC	or send an email to license@isb-sib.ch).						
DR	D90899; BA16579; 2;						
DR	InterPro:IP000092; Polyprenyl synt.						
DR	PFAM:PF00348; polyprenyl synt_1.						
DR	PROSITE:PS00444; POLYPRENYL SYNTHET_2;						
DR	PROSITE:PS00723; POLYPRENYL SYNTHET_1; FALSE NEG.						
KW	Photosynthesis; Isoprene biosynthesis; Transferase; Complete proteome.						
SQ	SEQUENCE . 323 AA; 35725 MW; 42160C6C165C685 CRC64;						
Query Match	30.8%; Score 676.5; DB 1; Length 323;						
Best Local Similarity	40.6%; Pred. No. 2.4e-39;						
Matches	153; Conservative 63; Mismatches 102; Indels 59; Gaps 4;						
Qy	65 LINPLNLVGP---EMSNITSNSSLGGPSLDTVAKKRILRPLVLLMVAQT 121						
Db	1 MISTTSILFAPVQODRLLTDNKRLVGAHPILGAAAEHLFEGGKRVRPAVLLVSRAT 60						
Query Match	30.8%; Score 676.5; DB 1; Length 323;						
Best Local Similarity	40.6%; Pred. No. 2.4e-39;						
Matches	153; Conservative 63; Mismatches 102; Indels 59; Gaps 4;						
Qy	65 LINPLNLVGP---EMSNITSNSSLGGPSLDTVAKKRILRPLVLLMVAQT 121						
Db	1 MISTTSILFAPVQODRLLTDNKRLVGAHPILGAAAEHLFEGGKRVRPAVLLVSRAT 60						

Db 62 EGNAHVIT -----AALEIFI 76
 QY 191 HAASLHDVVIDAESTRNAPSGNQAFGNKMAILAGDFLGRASVALRNRPEVELLA 250
 DR :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 77 HTATLHDVWESDMERGKATAFNGTAQASVLFYDFTYRAFMNTSISGLKLEUMS 136
 QY :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 251 TVIYALVVEGEFMQLNKNTVDATEATATOETFDYLYQKYLKTASLTAKSCRASALIGGAT 310
 DR :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 137 EAVNVIRAEVGVQLQMLVNNDPDI-----TEENYMRVIYSKTRARFEAAQCSGLAGCT 189
 QY :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 311 PVAADAAYAGVNLGLAQFOIVDMDLYTVSATDGLKGAGADOLQGATAPALFANKHAE 370
 DR :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 190 PBEKGILQDYGRYIGTAFOLIDDLYNDAGBQLGKNGDDLNNEGKPTPLHMHGT 249
 QY :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 371 LGPMIKRKFSDFGD---VERARELVKSDEKTRAEEYAQKALDAIRTPESPARK 426
 DR :|||:|||:|||:|||:|||:|||:|||:|||:
 250 EQAQMIERTAEGGNGRHLPEAMMAGCALSLEWTFQRABEADKAIAALQVLPDPWRE 309
 QY :|||:|||:|||:|||:|||:|||:|||:|||:
 427 ALFQLTDKVLTCSR 440
 Db 310 ALIGLAHIAVDR 323

RESULT 8

ISPB_HAEBIN STANDARD; PRT; 329 AA.

ID ISPB_HAEBIN STANDARD; PRT; 329 AA.

AC P49316; 1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update) Octaprenyl pyrophosphate synthetase (EC 2.5.1.-) (Octaprenyl pyrophosphate synthetase).
 DE ISPB OR H0081.

GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus influenzae.
 OC NCBI_TaxID=727;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95550630; PubMed=1542800;
 RA Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.P., Spriggs T., Heidelberg J., Portnoy D.T., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann N.S.M., Geochagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RA "Whole genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512 (1995).
 RT [2]
 RL IDENTIFICATION BY MASS SPECTROMTRY.
 RP MEDLINE=20137488; PubMed=10675023;
 RX Langen H., Takacs B., Evers S., Bernat P., Lahn H.W., Wipf B., Gray C., Fountoulakis M.;
 RA "two-dimensional map of the proteome of Haemophilus influenzae.", Electrophoresis 21:411-429 (2000);
 CC "-!- FUNCTION: SUPPLIES OCTAPRENYL DIPHOSPHATE, THE PRECURSOR FOR THE SIDE CHAIN OF THE ISOPRENOID QUINONES UBIQUINONE AND MENAQUINONE (BY SIMILARITY);
 CC "-!- SIMILARITY: BELONGS TO THE FPP/GCPP SYNTHETASES FAMILY.

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Db DR EMBL; U32770; AAC22540.1; --
 DR TIGR; H10881; -
 DR InterPro; IPR00092; Polypropenyl synt.
 DR PF00348; polypropenyl synt; 1.
 DR PROSITE; PS0044; POLY(2-ENYL)SYNTHET; 2; 1.
 DR PS00723; POLY(2-ENYL)SYNTHET; 1.
 DR Isoprene biosynthesis; Transferase; Complete proteome.
 KW SEQUENCE 329 AA; 35911 MW; 65DBC4CCDAB72E04 CRC64;

Query Match 20.3%; Score 445.5; DB 1; Length 329;
 Best Local Similarity 32.5%; Pred. No. 1; τ_e -23;
 Matches 119; Conservative 49; Mismatches 133; Indels 65; Gaps 6;

Db 66 -----GFEGSNSITCAT-----FVEFI 82

ISPB_HAEBIN STANDARD; PRT; 329 AA.

AC P49316; 1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update) Octaprenyl pyrophosphate synthetase (EC 2.5.1.-) (Octaprenyl pyrophosphate synthetase).
 DE ISPB OR H0081.

GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus influenzae.
 OC NCBI_TaxID=727;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95550630; PubMed=1542800;
 RA Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.P., Spriggs T., Heidelberg J., Portnoy D.T., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann N.S.M., Geochagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RA "Whole genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512 (1995).
 RT [2]
 RL IDENTIFICATION BY MASS SPECTROMTRY.
 RP MEDLINE=20137488; PubMed=10675023;
 RX Langen H., Takacs B., Evers S., Bernat P., Lahn H.W., Wipf B., Gray C., Fountoulakis M.;
 RA "two-dimensional map of the proteome of Haemophilus influenzae.", Electrophoresis 21:411-429 (2000);
 CC "-!- FUNCTION: SUPPLIES OCTAPRENYL DIPHOSPHATE, THE PRECURSOR FOR THE SIDE CHAIN OF THE ISOPRENOID QUINONES UBIQUINONE AND MENAQUINONE (BY SIMILARITY);
 CC "-!- SIMILARITY: BELONGS TO THE FPP/GCPP SYNTHETASES FAMILY.

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Db DR EMBL; U32770; AAC22540.1; --
 DR TIGR; H10881; -
 DR InterPro; IPR00092; Polypropenyl synt.
 DR PF00348; polypropenyl synt; 1.
 DR PROSITE; PS0044; POLY(2-ENYL)SYNTHET; 2; 1.
 DR PS00723; POLY(2-ENYL)SYNTHET; 1.
 DR Isoprene biosynthesis; Transferase; Complete proteome.
 KW SEQUENCE 329 AA; 35911 MW; 65DBC4CCDAB72E04 CRC64;

Query Match 20.3%; Score 445.5; DB 1; Length 329;
 Best Local Similarity 32.5%; Pred. No. 1; τ_e -23;
 Matches 119; Conservative 49; Mismatches 133; Indels 65; Gaps 6;

Db 66 -----GFEGSNSITCAT-----FVEFI 82

ISPB_HAEBIN STANDARD; PRT; 329 AA.

AC P49316; 1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update) Octaprenyl pyrophosphate synthetase (EC 2.5.1.-) (Octaprenyl pyrophosphate synthetase).
 DE ISPB OR H0081.

GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus influenzae.
 OC NCBI_TaxID=727;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95550630; PubMed=1542800;
 RA Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.P., Spriggs T., Heidelberg J., Portnoy D.T., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann N.S.M., Geochagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RA "Whole genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512 (1995).
 RT [2]
 RL IDENTIFICATION BY MASS SPECTROMTRY.
 RP MEDLINE=20137488; PubMed=10675023;
 RX Langen H., Takacs B., Evers S., Bernat P., Lahn H.W., Wipf B., Gray C., Fountoulakis M.;
 RA "two-dimensional map of the proteome of Haemophilus influenzae.", Electrophoresis 21:411-429 (2000);
 CC "-!- FUNCTION: SUPPLIES OCTAPRENYL DIPHOSPHATE, THE PRECURSOR FOR THE SIDE CHAIN OF THE ISOPRENOID QUINONES UBIQUINONE AND MENAQUINONE (BY SIMILARITY);
 CC "-!- SIMILARITY: BELONGS TO THE FPP/GCPP SYNTHETASES FAMILY.

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DR EMBL; D49976; BAA00092; Polyprenyl synt.

DR InterPro; IPD00092; Polyprenyl synt; 1.

DR PROSITE; PS0044; POLYPRENYL SYNTHET_2; 1.

DR PROSITE; PS00723; POLYPRENYL SYNTHET_1; 1.

KW Isoprene biosynthesis; Transferase.

SQ SEQUENCE 320 AA; 35808 MW; A51B6530E6B88F46 CRC64;

Query Match 18.6%; Score 409; DB 1; Length 320;

Best Local Similarity 28.5%; Pred. No. 5e-21; Matches 106; Conservative 61; Mismatches 127; Indels 78; Gaps 6;

Qy 70 NLVGPMSNLTSNRLSLGSHPSDLTVAKKYYQSEGRHIRPLMVLLMAQATEVAPKVQG 129

Db 8 SFSLDDLAVEEELERAVQSEYGPLGEAHLHQAGGKRIRPVFLLAARP----- 58

Qy 130 WEKVVVEVPVNEGLAPPEVILNDKPNPDMMMNRSGPLTKDGBIEGOTSNTILASORRRAEITEM 189

Db 59 ----- GOVD--LERMHVAEAL 75

Qy 190 THAASLHDDVIDASETTRRNAPSGNQAFGNKMAILLAGDFLLGRASVALARLNPEVIELL 249

Db 76 IIMASLHVHDVIDADLURGRPTIKAKWSNRFAMYTGYLFASLERNMAELGNPRAQVL 135

Qy 250 ATIVANLVVEGEFMOLKNTVDDATEATAQTETFDY---YLOKTYLKTAASLIAXSCRASAL 305

Db 136 AKTIVEVRGEIQLKD-----KYRFDOPLRTYLRIRRKPALLIAASCQLGAL 184

Qy 306 LGGATPEVADAAYAGRNLGAFOIQVDDMLDTYTSATDLKGPKAGDLOGLLTAPALFAW 365

Db 185 AGAAPEPTVKRLTWFGHTVGMSSFTIDDLFTCTEBOLKGPKGSDLQGNTLPVLYAL 244

Qy 366 KHH-----AEIGPMIKRKPSDPCDVARELEYKSDGLEKTTAALAEYAAQXQDARTF 419

Db 245 SDERVKAALAAVGEE----TDVAAEMAAVISALKRTDAIERSVALSDRYLDKALHLLDGL 299

Qy 420 PESPARKALEQL 431

Db 300 PMNEARGLRLD 311

RESULT 10

ID HEPB_BACSU STANDARD; PRT; 348 AA.

AC P31114;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Heptaprenyl diphosphate synthase component II (EC 2.5.1.30) (HEPPP)

DE synthase subunit 2 (Spore germination protein C3).

GN HEPT OR HEPB OR GERCC OR GERCS3.

OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

[1] NCBI_TAXID=1423;

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RA Henner D.J.;

"Sequence of *Bacillus subtilis* dbPA, mtr(A,B), gerC(1-3), ndk, cher,

aro(B,E,F,H), trp(A-F), hisH, and tyrA genes."

RT Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.

[2] CHARACTERIZATION OF GERC LOCUS.

RP MEDLINE=91037938; PubMed=2121900;

RA Yazdi M.A.; Moir A.;

"Characterization and cloning of the gerC locus of *Bacillus subtilis*

168.;"

J. Gen. Microbiol. 136:1335-1342(1990).

[3] FUNCTION.
RN [REMOVED]; Published=9720033;
RP

RX MEDLINE=98316502; "The gerC locus of *Bacillus subtilis*, required for menaquinone synthesis, is concerned only indirectly with spore germination."

RA Leatherbarrow A.J.H.; Yazdi M.A.; Curson J.P.; Moir A.;

RT "The gerC locus of *Bacillus subtilis*, required for menaquinone synthesis, is concerned only indirectly with spore germination."

RL Microbiology 144:2125-2130(1998).
CC -1- FUNCTION, SUPPLIES HEPTAPRENYL DIPHOSPHATE, THE PRECURSOR FOR THE SIDE CHAIN OF THE ISOPRENOID QUINONE MENAQUNIONE-7 (MQ-7).

CC -1- CATALYTIC ACTIVITY: All-trans-heptaprenyl diphosphate + isopentenyl diphosphate = diphosphate + all-trans-heptaprenyl diphosphate.

CC -1- SUBUNIT: HETERO-DIMER OF COMPONENT I AND II.
CC -1- SIMILARITY: BELONGS TO THE FPP/GPP SYNTHETASES FAMILY.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@sb-sib.ch).

CC CC DR M80245; AAA20856; 1.;

DR DR EMBL; 299117; CAB14190; 1.;

DR DR Subtilist; BG10281; heptT.

DR DR InterPro; IPR00092; Polypropenyl synt.

DR DR Pfam; PF00348; Polypropenyl synt; 1.

DR DR PROSITE; PS00444; POLYPRENYL SYNTHET_2; 1.

DR DR PROSITE; PS00723; POLYPRENYL SYNTHET_1; 1.

KW Sporulation; Isoprene biosynthesis; Transferease; Complete proteome.

SQ SEQUENCE 348 AA; 39515 MW; OFG9C9199FFB04BE CRC64;

Query Match 18.5%; Score 406; DB 1; Length 348;

Best Local Similarity 27.0%; Pred. No. 9.1e-21; Matches 101; Conservative 69; Mismatches 125; Indels 70; Gaps 6;

Qy 70 NLVGPMSNLTSNRLSLGSHPDSLTDVAKYYQSEGRHIRPLMVLLMAQATEVAPKVQG 129

Db 36 SFNDDIVIERLEQTVRSDFPLLSAGLHLQAGGRIRPFLVFL----- 82

Qy 130 WEKVVVEVPVNEGLAPPEVILNDKPNPDMMMNRSGPLTKDGBIEGOTSNTILASORRRAEITEM 189

Db 83 -----SCMF-----GDYD-----INNKIVVAVTLEM 103

Qy 190 THAASLHDDVIDASETTRRNAPSGNQAFGNKMAILLAGDFLLGRASVALARLNPEVIELL 249

Db 104 IIMASLHVHDVIDADLURGRPTIKAKWSNRFAMYTGYLFASLERNMAELGNPRAQVL 135

Qy 130 WEKVVVEVPVNEGLAPPEVILNDKPNPDMMMNRSGPLTKDGBIEGOTSNTILASORRRAEITEM 189

Db 190 THAASLHDDVIDASETTRRNAPSGNQAFGNKMAILLAGDFLLGRASVALARLNPEVIELL 249

Db 164 SQTIVELVGEFWMQLNTVDDATEATATQETFDYILOKTYLKTAKSSCRASALIGGA 309

Qy 250 ATIVANLVVEGEFMQLNTVDDATEATATQETFDYILOKTYLKTAKSSCRASALIGGA 309

Db 164 SQTIVELVGEFETQIKDYN-----MEQNRTYLERI-KRKTALLITAVSCQGATAGA 216

Qy 310 TPEVADAYAYGENLGFQIVYDMDLYTVAATDLGKPGADLQLGLATAPALFWKHA 369

Db 217 DERIKHALYWFQYVGMSYQIIDDLDFTSTEBELGPVGDDLQGNTVLPVLYALRN-- 274

Qy 370 ELGPBMKRF-----SPGDYVERAREVRSGLKEKRALABEYAKDALDRAFTFPBPSP 423

Db 275 ---PALXNQLKLINSETTQEQLEPIEEIKTKDAIEASMAVSEMYLQKAQKLINTLPRGR 331

Qy 424 ARKAL 428

Db 332 ARSSL 336

RESULT 11
IDSA_MEETH
ID _IDSA_MEETH
ID AC O2156;
AC DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bifunctional short chain isoprenyl diphosphate synthase [Includes:
 DE Farne'sl pyrophosphate synthetase (EC 2.5.1.1) (FPP synthetase)
 DE (Dimethylallyltransferase); Geranyltranstransferase (EC 2.5.1.10).
 GN IDSA OR MTHS0.

OS Methanobacterium thermoautotrophicum
 OC Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 NCBI_TaxID=187420;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN-Delta H;

RX MEDLINE=98037514; PubMed=9371463;

RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Hoang D., Harison D., Hoang L., Keagle P., Lunn W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwanji N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nuelle J., Reeve J.N.; RT DeltaH: functional analysis and comparative genomics.;"
 RL Bacteriol. 179:7135-7155(1997).

CC -!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diposphorylethylene + Geranyl diphosphate.
 CC = diposphorylethylene + trans-trans-farnesyl diphosphate.
 CC -!- COFACTOR: REQUIRE MAGNESIUM.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Cyttoplasmic.

CC -!- SIMILARITY: BELONGS TO THE FPP/GPP SYNTHETASES FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AE000197; AAB84557.1; -

CC DR InterPro; IPR00092; Polypropenyl synt.
 DR Pfam; PF0348; Polypropenyl synt.
 DR PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

CC DR PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
 CC Lipid Synthesis; Isoprene biosynthesis; Transferase; Magnesium; KW Multifunctional enzyme; Complete proteome.

SQ SEQUENCE 325 AA; 35485 MW; BCF3A285A207916E CRC64;

Query Match 16.7%; Score 365.5; DB 1; Length 325;
 Best Local Similarity 29.3%; Pred. No. 4.9e-18; Matches 109; Conservative 61; Mismatches 133; Indels 69; Gaps 9;

QY 75 EMSNLTSNRSLIGGSHP-SLPTVAKYYVQSRRGHKRPLMVIMAOATEVAPVKVQCGWEKU 133

Db 13 ERAD--ERIESIDITPETILLRASEHLITAGKKRIPSLANLISSEAVGGDP----- 62

QY 134 VEVPPNEGLAPPEVLNDKNPDMAMMRSGPLTKDGELEGOTSNILASQRRAEITEMHAA 193

Db 63 -----GDAG-----VAAEELIHTF 78

QY 194 SLLHDVVIDASERRNAPSGNQAFGNKMAILLAGDFLGRASVALRNLNPVI-ELIATV 252

Db 79 SLIHDIMDDEIRRGSPAHVILWGERMAILAGDVLFPSKAFAEVIRGDSEMVKALAVV 138

QY 253 IANTLV--EGERNQKQVVDAA-TTOEFDYVQLOQTYKTTASLJAKSCRASALLGA 309

Db 139 VDSCVKICEQALDM--GFEERLDVTE-----YMEMYKRTAALIAAKAGAIAGGG 191

QY 310 TREVADAYAIGRNGLAQFOVDDMLDVTSAIDLGRPAGDLQLQGLATAPALPKHHA 369

Db 192 SPQETAALEDYGRCIGLAFOHDDYLDVWSDEESLGKPVGSIDAEGRNTLNVKALERAS 251

QY 370 ELGPMIKRKFSDFPGD--VERARELVEKSDGLEKTRALAAEYAAQKALDAIRTFFPSSPARK 426

RESULT 12

IDSA_METTM IDSA_METTM STANDARD; PRT; 324 AA.

AC 053479; 01-NOV-1997 (Rel. 35, Created)

DT 15-JUL-1998 (Rel. 36, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Bifunctional short chain isoprenyl diphosphate synthase [Includes:
 DE Farne'sl pyrophosphate synthetase (EC 2.5.1.1) (FPP synthetase)
 DE (Dimethylallyltransferase); Geranyltranstransferase (EC 2.5.1.10).
 GN IDSA.

OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).

OC Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.

NCBI_TaxID=79929;

RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=95070145; PubMed=7979381;

RA Chen A., Poultier C.D.; "Isolation and characterization of idsa: the gene for the short chain isoprenyl diphosphate synthase from Methanobacterium thermoautotrophicum"; RLT Arch. Biochem. Biophys. 314:399-404(1994).

CC -!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diposphorylethylene + Geranyl diphosphate.

CC -!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diposphorylethylene + trans-trans-farnesyl diphosphate.

CC -!- COFACTOR: REQUIRE MAGNESIUM.

CC -!- SUBUNIT: HOMODIMER.

CC -!- SUBCELLULAR LOCATION: Cyttoplasmic.

CC -!- SIMILARITY: BELONGS TO THE FPP/GPP SYNTHETASES FAMILY.

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CC EMBL; S75695; AAB32421.1; -

CC DR InterPro; IPR00092; Polypropenyl synt.
 CC DR Pfam; PF0348; Polypropenyl synt.
 DR PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

CC DR PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
 CC Lipid synthesis; Isoprene biosynthesis; Transferase; Magnesium; KW Multifunctional enzyme.
 FT INIT MET 0

SQ SEQUENCE 324 AA; 35505 MW; 88558AE4DF5F66C1 CRC64;

Query Match 16.5%; Score 331.5; DB 1; Length 324;
 Best Local Similarity 31.4%; Pred. No. 9.2e-18; Matches 107; Conservative 58; Mismatches 134; Indels 42; Gaps 8;

QY 121 TEVAPKVQGWEKVEVPNEGGLAPPEVLNDKNPDMAMMRSGPLTKDGELEGOTSNILAS- 179

Db 1 TEVIDLRLKVEVADKRI-----MECISDITPDTLKASEHLITAGKKRIPSLANLSC 54

QY 180 -----QRLLAEITMIHAA-SLLHDVMDVIASETERRNAPSGNQAFGNKMAILAGDFL 230

Db 55 EAVGNGPDAAGVAAEILHTSLLHDIMDDEMARGERSVHVINCEPHMILAGVLF 114

QY 231 GRASVALRNLNPB-VIELLATVIANLV--ECEFPMLKNTVDATEBATOBTFDYLQ 286

Db 115 SKFAEAVRNLNPB-VIELLATVIANLV--ECEFPMLKNTVDATEBATOBTFDYLQ 167


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Db 138 AFSIFITSIEIISSEGQAMDMSFENRLD-----VTEEE---YIQMIGKKTAMLFSCSAAL 1.88
Qy 303 SALGGATEPEVADAYAAGRNLGIAFQIVDDMLDYTVSATDLSKPGAGDLQQLATAPAL 362
Db 189 GGLINKANDDVKKLTVEGLNLGSFQIVDDILIGIDKELGKPTYSIREGKKTILVI 248
Qy 363 FAWKHAE---LGPMITKRFDSPGDUVERARELVEKSGLBEXTRALAEEYAOAKDAIR 417
Db 249 KTLSEATEDEKKILVSTLGNKEAKKEDLERASEEIRK-HSLQAYDLAKKYSDLAIENLR 107
Qy 418 TFPES--PARKALEBOLTDKVLTCSR 440
Db 308 EIPVSNKTAEKALKYLAQFTIQRK 332

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Search completed: January 16, 2003, 09:49:01
 Job time : 24 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 16, 2003, 08:53:11 ; Search time 67 Seconds
(without alignments)
1353.145 Million cell updates/sec

Title: US-09-830-111A-2
Perfect score: 2194
Sequence: 1 MASPALIRSISSRSTASLR..... ESPARKALEQLTDKVYLTRSR 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206407115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*

1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
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QY	187	TEMTIHAASLILDDVIVDASSETTRAPASPGHQAFGKMAILLAGDFELGRASVALRNPEVI	246	DR
				DR
				FlyBase; FGDN003984; CG3684.
Db	126	TEMTHIASLILDDVIVDHNVRGRSPSSNWFGNRSLIGANFLARASTVMARLNPOVT	185	DR
				InterPro; IPR00092; PolyPrenyl-synt.
QY	247	ELATIVIANLVESEPMQLKNTVDAEATATQTFDYLQKYLKTASLIAASCRAAL	306	DR
				Pfam; PF00448; PolyPrenyl-synt.
Db	186	ELATIVIALDVLRGFQLQKNTMOP-SLEIKQSNFDVYIYEKSFLKTAASLISKCASTIL	244	DR
				PROSITE; PS00444; PolyPrenyl-Synthet-2; 1.
QY	307	GGMPPEVADAYAVGRNGLAQFTVDDMDLYTWSATDGKPGACDOLQGLATAPALFAWK	366	DR
				SEQUENCE; 430 AA; 48759 MW; 3CF533C8C6F03029 CRC64;
Db	245	GQCSPTVATAGYGRCGTAFQLMDDVLDYTSKDDTIGKAAGADLKGLATAPVLFWK	304	DR
				SBQUENCE; 430 AA; 48759 MW; 3CF533C8C6F03029 CRC64;
RESULT 2				
QSV923		PRELIMINARY;	PRT;	430 AA.
ID	QSV923;			
AC	QSV923;			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	CG3684	protein.		
GN	CG3684	Drosophila melanogaster (Fruit fly).		
OS	Drosophila melanogaster			
OC	Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Ephydryoidea; Drosophilidae; Drosophila.			
OC	NCBI_TaxID=7227;			
RN		SEQUENCE FROM N.A.		
RP		STRAIN-BERKELEY;		
RX		MEDLINE:2019-0006; PubMed:10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Suttorp G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Branden R.C., Rogers Y.-H.H., Blazej R.G., Champé M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Heltz G., Nelson C.R., Miklos G.L.G.,			
RA	Abrii J.F., Agbayani A., An H.-J., Andrews P, Frankkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,			
RA	Benson K.Y., Benos P.V., Berman B.P., Bhardwaj D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Broctier P.,			
RA	Burts K.C., Busam B., Butler H., Cadieu B., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahibe C., Davenport L.B., Davies P.,			
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,			
RA	Glodek A., Gong F., Goorell J.H., Gu Z., Guan P., Hairs M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Illegwan C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherf A.,			
RA	Mourt S.M., Moy M., Murphy B., Murphy L., Muñoz D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskeen D.R., Pacieb J.M.,			
RA	Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Rubin H., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Yers R.A., Myers E.W., Venter J.C.,			
RA	The genome sequence of Drosophila melanogaster.;			
RP		SEQUENCE FROM N.A.		
RA	Zimmer W., Oschinski C.,			
RT	"Identification of a prenyl transferase gene from Quercus robur."			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDJB databases.			
DR	EMBL: AU290245; CACTUS0852_1;			
DR	InterPro: IPR000092; PolyPrenyl			
DR	Pfam: PF00448; PolyPrenyl_synth_1;			
DR	PROSITE: PS00444; PolyPrenyl_Synthet_2_1;			
DR	SEQUENCE: 416 AA; 46243 MW; 2914B2D071680AFL CRC64;			
Query Match				
QY	33.8%	Score 742; DB 5; Length 430;		
QY	33.7%	Best Local Similarity 37.2%; Pred. No. 4.2e-43;		
Db	167	Matches 167; Conservative 85; Mismatches 135; Indels 62; Gaps 6;		
QY	3	SPALRIRS-SRSIASLR---SMTLTAPSRLRCPSTSPPSSWAAVASSARIV	57	QY
Db	112	TMVMLMAKANY-----HLNN 168	228	Db
QY	33	ARGYTINHIELTESKSVRLOOPSATKESTISVYQSFHKCSQSLQISQSSKANLQRHHV 92	228	QY
QY	58	ERDPNQPL---INPINLVGPEMSVNTSNSLGS-HPSLDVAKYVQSGKHP 111	231	Db
Db	93	TQQPAGPVRFQIDPYTILDLYKYYFDVYLLKGTSQPELDITASYFDDGCKALRP 152	231	QY
QY	112	IMVLLMAQATEVAPKVQGWEKVEVNEVNEGLAPPVNLNDKNPDMNMRSQPLTKGEIEG 171	231	Db
Db	153	MVTMILMAKANY-----HLNN 168	228	QY
QY	172	QPSNIALSASORLAETEMTHIASLILDDVDASEPRRNAVSNGNQDAGFGNKWAIIAGDFLUG 231	231	Db
Db	169	ESHQLVHKQROJALFSEMWHSASLVLDDVLDOSDFRKGPSVNALWNHKKVTMAGDYL 228	228	QY
QY	229	IASIMARLRSDDVVLSQSLTDVVOGEFMQSGSRETE-----NERFAHVLTKTYRK 281	228	Db
QY	292	TASLIKSKCRASALLGCATPEVADAYAVGRNGLQAFQTVDDMDLYTWSATDGKPGAD 351	351	QY
Db	282	TASLIKSKATAVIAQADNVVAEYAOYERNIGLAQFQVDDMDLFVFSSTEOMGKPTAAD 341	341	Db
QY	352	IQLGILATAPALPAFKWAHELGPMKIRKFSPGDVVERARELVEKSGQLEKTRALAEYAK 411	411	QY
Db	342	LKGILATAPVLFACYPCEPVLNPVMVRFRSFSGDVERAFELVHKSHGLEQTFLAKKHNE 401	401	Db
QY	412	ALDAIRFPPESPARKOLEQDVKVLSR 440	440	QY
Db	402	AIRLAQBLTESPYQKJLQVQVADLVRINRMK 430	430	Db
RESULT 3				
QPFET8		PRELIMINARY;	PRT;	416 AA.
ID	QPFET8			
AC	QPFET8;			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Geranyl diphosphat synthase.			
GN	GPS.			
OS	Quercus robur (English oak)			
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Rosidae; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids II; Fagales; Fabaceae; Quercus.			
OX	Quercus robur			
QY	1	QPFET8; Polyprenyl_synth_1;	38942;	QY
RN		SEQUENCE FROM N.A.		
RA	Zimmer W., Oschinski C.,			
RA	"Identification of a prenyl transferase gene from Quercus robur."			
RA	Submitted (JUN-2001) to the EMBL/GenBank/DDJB databases.			
DR	EMBL: AU290245; CACTUS0852_1;			
DR	InterPro: IPR000092; PolyPrenyl			
DR	Pfam: PF00448; PolyPrenyl_synth_1;			
DR	PROSITE: PS00444; PolyPrenyl_Synthet_2_1;			
DR	SEQUENCE: 416 AA; 46243 MW; 2914B2D071680AFL CRC64;			

Best Local Similarity Matches 161; Conservative 41.8%; Pred. No. 1.4e-42;	Pred. No. 1.4e-42; Mismatches 92; Indels 56; Gaps 6;	Db 125 KQFRSTILLMATAV-----RVEALIGESTDIV----- 155
Qy 67 NPNPLVGPFEMNTSNRSLLGGHPSLDTVARYYVS--BKRHIRPLMLVLMQAQTEVA 124	Qy 167 GBIEGOTSNILASORRLAEITEMIHASLIIHDVIDDASETTRNAPGNGQAFGNKMAILAG 226	
Db 77 DPPSLVADLSWAVANRLSRMSVTVTVPKLASAAYFFKMGVEGKFRFTVLLIMATANNIS 136	Db 156 -----TSELVRQRGIAITEMIHASLIIHDVIDDASETTRGVSLSNVNGNKNHSVLG 209	
Qy 125 -- PKVQGWKEVYEVPVNEGGLAPEVNLNDKPNDDMMNRSGPLTKDGTEGOTSNILASQR 181	Qy 227 DFLGRASVALARLNPEVIELLATVIANLYVEGEFMOLKNTVDDATEATAQETFDYLLQ 286	
Db 137 1LEPSLRQ-----PGDAL-----TELDARQQ 158	Db 210 DFLSRAGALAAKNTEVALLATAVEHLVTGETNEITS-----SSTERGYSMYYMQ 262	
Qy 182 RLAEITEMIHASLIIHDVIDDASETTRNAPGNGQAFGNKMAILAGDFLGRASVALARL 241	Qy 287 KTYLKTAISLIAKSCRASALLGATPVEADAAYAGRNLGLAQIYDDMDYTVSATDGLK 346	
Db 159 RAEEITEMIHASLIIHDVIDDADTTRGIGSLNFVMGNKLAVLAVGDLPSRACVALASLK 218	Db 263 KTYKTAISLNSCRASAKVALTGQTALAVLAFFEYGRNLGLAQIYDDMDYTVSATDGLK 322	
Qy 242 NPEVIELLATVIANLYVEEPMQLKNTVDDATEATAQETFDYLLQKTYLKTAISLIAKSCR 301	Qy 347 PAGADLOGLATAPALAWKHAELGPMPMRKFSDPGEVARELVEKSQDGLIEKTALAE 406	
Db 219 NTENVSVSLLAKVVEHVLVLTGETQMOMTTCEORC-----SMEYTMQRTYYKZTLNSNSCK 271	Db 323 GSLSLDIRHGVTAPILFAMEEFPQLREVQDVEKOPRNVDALLEYLGSKGIORARELAM 382	
Qy 302 ASAILGGATPEVADAAYAGRNLGLAFOIVDMDDYTVSATDGLKPAGADUQGLATAPA 361	Qy 407 EYAOKALDAITRFPESP-----ARKALEQLTDKVLTCSR 440	
Db 272 AIAILGGQTSEVANLAYYGRNLGLATOLIDVEDFTGTSASLGKGSLSUDRHGJITAPI 331	Db 383 EHANLAAAAGSLPETDNEDVRSRALIDDTHRVITRNC 422	
Qy 362 LFAWKHHAELGPMIKRKFSDFPGEVERALEVKSQDGLEKTRALAEEYAQAKALDAITRFPS 421		
Db 332 LFAMEEFFPQLRETVYDGFDDPANVYDPAVQDYLGSRSQRGIORARELAKHANIAEADSYPE 391		
RESULT 5		
QBRWML ID QBRWML PRELIMINARY; PRT; 423 AA.	AC QBRWML PRELIMINARY; PRT; 423 AA.	
QY FT89 ID QBRWML PRELIMINARY; PRT; 422 AA.	AC QBRWML PRELIMINARY; PRT; 423 AA.	
AC Q9FT89; DT 01-MAR-2001 (TREMBLrel. 16, Created)	AC QBRWML PRELIMINARY; PRT; 423 AA.	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
RN [1]	DE Putative trans-prenyltransferase.	
GN AT2G4630.	GN Arabidopsis thaliana (Mouse-ear cress).	
RP Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,	OS Arabidopsis thaliana (Mouse-ear cress); Streptophyta; Embryophyta;	
AC Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,	OC Spermatophyta; Magnoliophyta; Magnoliophyta; eudicots; Rosidae;	
OC Kim C., Lin J., Liu S.X., Naruseoka M., Pham P.K., Sakano H.,	OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
OC Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,	OX NCBI_TaxID=3702;	
CX Ecker J., Theologis A., Davis R.W.;	RN	
DR Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	RP SEQUENCE FROM N.A.	
DR DR ENBL; AX093006; AACM13005.1; -.	RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,	
DR RN	RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,	
DR DR 01-MAR-2001 (TREMBLrel. 16, Created)	RA Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,	
DR DR 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	RA Kim C., Lin J., Liu S.X., Naruseoka M., Pham P.K., Sakano H.,	
DR DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,	
DR DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	RA Ecker J., Theologis A., Davis R.W.;	
DR DR Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	GN Arabidopsis thaliana (Mouse-ear cress).	
DR DR DR ENBL; AX093006; AACM13005.1; -.	OS Arabidopsis thaliana (Mouse-ear cress); Streptophyta; Embryophyta;	
DR DR DR RN	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
DR DR DR OC	OC Spermatophyta; Magnoliophyta; Magnoliophyta; eudicots; Rosidae;	
DR DR DR OC	OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
DR DR DR CX	OX NCBI_TaxID=3702;	
DR DR DR RN	RN	
DR DR DR RX	RP SEQUENCE FROM N.A.	
DR DR DR RA	RA Bouvier F., Suire C., D'Harlange A., Backhaus R., Camara B.,	
DR DR DR RT	RT "Molecular cloning of geranyl diphosphate synthase and	
DR DR DR RT	RT compaction of monoterpane synthase in plant cells";	
DR DR DR Plant J. 24:241-252 (2000)	Plant J. 24:241-252 (2000)	
DR DR DR EMBL; Y17376; CAC16849.1; -.	DR EMBL; Y17376; CAC16849.1; -.	
DR DR DR InterPro; IPR000092; Polypropenyl synt.	DR InterPro; IPR000092; Polypropenyl synt.	
DR DR DR PROSITE; PS00348; Polypropenyl synt; 1.	DR PROSITE; PS00348; Polypropenyl synt; 1.	
DR DR DR PROSITE; PS00723; POLYRENYL SYNTHET_1; 1.	DR PROSITE; PS00723; POLYRENYL SYNTHET_1; 1.	
DR DR DR SEQUENCE; 422 AA; 46402 MW;	DR SEQUENCE; 422 AA; 46402 MW;	
DR DR DR SQ	DR SQ SEQUENCE; 422 AA; 46402 MW;	
DR DR DR	DR DR DR Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps 9;	
DR DR DR	DR DR DR Query Match 32.4%; Score 710.5; DB 10; Length 422;	
DR DR DR	DR DR DR Best Local Similarity 38.5%; Pred. No. 6.1e-41;	
DR DR DR	DR DR DR Matches 177; Conservative 84; Mismatches 132; Indels 67; Gaps	

RN [3]	SEQUENCE FROM N.A.
RP	
RC	STRAIN-BRISTOL N2;
RA	Waterson R.;
RT	"Direct Submission";
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; U80443; AA337678.2; -.
DR	IntePro; IPR000992; Polypropenyl synt.
DR	Pram; PFO348; Polypropenyl synt; 2.
DR	PROSITE; PS0044; POLYPRENYL_SYNTHET_1; 2.
DR	KW Hypothetical protein.
SEQUENCE	393 AA; 43003 MW; 4C5FC2EAC87EB5E2 CRC64;
Query Match	29.2%; Score 641.5; DB 5; Length 393;
Best Local Similarity	36.7%; Pred. No. 3.1e-36;
Matches	153; Conservative 51; Mismatches 125; Indels 65; Gaps 9;
QY	39 TSPRSSSSWAAYVSSAS-----RLVEPDNPQPLINPLNLPGPEMSNLTSNTI 83
QY	22 TSTTSSSDNSVASTAFWQEHVRQMQNDIMVQLIPQDSEGAVENTADL----NVTSN- 74
QY	84 RSLIGSGHPSLDTVAKYVYVOSGKHTIRPLMVLMAQTEVAPKVQMEKVYEVPNNEGLA 143
Db	75 -----LGRMTHYYFOQQGSKMLRPTVSLIMGNACNSAANRSTSBEYLAMLSTE-- 121
QY	144 PPEVLNDKNPDMNMRSQPLTKDGEIGEQTSNLLASQRRLABITEMTHAASLHDVDA 203
Db	122 -----RSG-----IAAHLs-VCQNYKIGMIAEMHTASLHVDDIVE 158
QY	204 SETTRNAAGSGNQAFGNKNAVAILAGDFLGRASVALARLNPEVIELATVIANLVEGEFMQ 263
Db	159 ANTRRGSAVSNAVWGNKMSVLFILARATQILCSIGKPNISVMASIDLVGEFMQ 218
QY	264 LKNTVDADEATATQEFDDYVYQKTYLKTAJAKSRSASALIG-GATPEVADAYAGR 322
Db	219 MSTPTPTADTPV---DRMKAYIBKTHRKTASLFASSCRSAATLADGSDLKHAEFAYGR 274
QY	323 NUGLAQTVDDMDLDTYSATDICKPAGDOLQIGLATAPALFKWKKHAEGLGMIKRFSDP 382
Db	275 NUGIAFQIADDLDFIATADEMGKPVADLKGLATAFPLVACEQPFLNLMLRKPHD 334
QY	383 GDVERABSLVEKSDGLEKTRALAEYAKALDAIRTFPESPARKAIBQLTDKVTRS 439
Db	335 GDAEKAREIVVNNSDGMKTRRLIDSYSQKAVEMASSLUPN-RNESTEHLIKAMQS 389
RESULT	11
OBSY08	PRELIMINARY; PRT; 245 AA.
ID	QSY08;
AC	QSY08;
DT	01-JUN-2002 (TREMBlrel. 21, Created)
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	Polypropenyl diphosphate synthase.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1] SEQUENCE FROM N.A.
RC	STRAIN=CV. COLOMBIA;
RA	Hirooka K., Fukusaki E., Kobayashi A.;
RT	"Polypropenyl diphosphate Synthase Involved in Quinone Biosynthesis from Higher Plant.";
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AB071514; BAB895941.1; 2FDDDI187A569411 CRC64;
SEQUENCE	406 AA; 44468 MW;
QY	Query Match 25.7%; Score 585; DB 10; Length 406;
Best Local Similarity	33.6%; Pred. No. 2.6e-32;
Matches	135; Conservative 69; Mismatches 140; Indels 58; Gaps 5;
DE	REB374P;
GN	C03684.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydriidae; Diopsophilidae; Drosophila.
OC	NCBI_TaxID=227;
RN	[1] SEQUENCE FROM N.A.
RP	STRAIN-BERKELEY;
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,' George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,' Miranda A., Mungall C.J., Nuno J., Pacleb J., Paregas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celikiner S.;
RA	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY07563; AAL68276.1; -.
SEQUENCE	245 AA; 27384 MW; 66CCD7DD5A8A3A1D CRC64;
QY	150 DKNPDMNMRSQPLTKDGEIGEQTSNLLASQRRLABITEMTHAASLHDVDASETRR 209
Db	141 -----ABLG-L-KLELTTEHRRLABITEMHTASLHDVDAESMRG 182
QY	210 APSGNQAFGNKMAVIALAGDFLGRASVALARLNPEVIELATVIANLVEGEFMQ 269
Db	183 KETWHELFCTRVAVLAGDFPMQAWSVLYENLEVKLISQVKIDPASEKQASLFD 242
QY	270 DATEATATQEFDDYVYQKTYLKTAJAKSRSASALLGGATEVADAYAYORNGLAQ 329
Db	243 -----CDTKLDEYLKSFYKIASLVAESTKGAAIFSRVERDVTEOMIEFGKNGLGSFQ 295

Qy	330	IYDDMLDYTVSATDLGKPGAGADLQLATAPALFAMWKHAELEGPMIKRKFSUPGDFVERAR	389		RESULT 14
Db	296	IYDDILDQTGSTSQLGKPGASDIAKGNTTAPITFALREPRELIIESEFCAGSLEAI	355	Q9SHG4	PRELIMINARY;
Qy	390	ELVEKSDGLEYTRALAAEYAAQVALDAARTFPSPARKALEQL	431	ID Q9SHG4;	PRT;
Db	356	EAVTKGGGSIKRQELAREKAQDAIKNUCLPSPGSFRSALEM	397	AC Q9SHG4;	379 AA.
				DT 01-MAY-2000 (TREMBLrel. 13, Created)	
				DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
				DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
				DE Very similar to preynt transferase.	
				GN F20D23_25.	
				OS Arabidopsis thaliana (Mouse-ear cress).	
				OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
				OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
				OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
				OX NCBI_TAXID=3702;	
				RN [1]	
				RP SEQUENCE FROM N.A.	
				RC STRAIN=CV_COLUMBIA;	
				RA Fedderspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,	
				RA Araujo R., Huizar L., Buehler E., Dunn P.,	
				RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,	
				RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,	
				RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaya V.S.,	
				RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,	
				DR Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
				DR EMBL; AC007651; AAD5005_1; -;	
				DR InterPro; IPR000092; Polyprenyl synt.	
				DR Pfam; PF00348; Polyprenyl synt.	
				DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.	
				DR PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.	
				KW TRANSFERASE;	
				SEQUENCE 379 AA; 41916 MW; AC07C095915D9B9E CRC64;	
				Query Match 26.2%; Score 574.5; DB 10; Length 379;	
				Best Local Similarity 35.2%; Pred. No. 1.2e-31; Gaps 3;	
				Matches 127; Conservative 66; Mismatches 115; Indels 53;	
				Qy 71 LVGPENSNLTNSRSLIGSGHPSLDTYAKYYVQSEGKHIRPLVLLMAQATEVAPVQGW 130	
				Db 63 VVADDLQRNDNLISIVGAENPVLSAEEQIFSAGGSKRMRLGVFLVSRAT----- 113	
				Qy 131 ERKVEVPVNEGLAPPVLDNKNPDMNMRRSGPLTKDQEGETSNLTASQRLAETEMI 190	
				Db 114 ----- 136	
				----- AELAG_LKELTVEHRLRGTEIMI 136	
				Qy 191 HAASLLHDVIDDADSETTRNAPSGNQAFGNKMAILAGDFFLGGRASVALARLNPEVIELLA 250	
				Db 137 HTASLTHDVIDDDESMDNRGREYHELFGTRYAVLAGDFMFQAWSYLNLNEVKLIS 196	
				Qy 251 TVIANLVGEFNMQLKNTVDDALEATATQETPDYLYOKTYLTASLIAKSRSASALLGGAT 310	
				Db 197 QVIKDFASGE1KQASSIFDCDVK-----LDDYMLKSYXTASLVAASTGAAIFSKVE 249	
				Qy 311 PEVADAYAYGRNLGAFOIQIVDDMLDYTVSATDLGKPGADQLQGLIATAPALFAWKHAE 370	
				Db 250 SKVABQMYQFGNKLGLSQVQDILDEFQSTBQLGRPANDLAKGNTAPTFALENEPR 309	
				Qy 371 LGPMIKRKFSFDPGDVERARELVEKSQDGLEKTRALAEAYAQKALDAIRTPESPARKALEQ 430	
				Db 310 LREIIIESFCFGSLSPEEAIEVRNREGGIIKRAQELAKEKAELALKNCINCLPRSGFRSALEM 369	
				RESULT 15	
				Qy 431 L 431	
				Db 370 M 370	
Qy	175	NILASORRLAETITEMIHAASLHDDVIDDADSETTRNAPSGNQAFGNKMAILAGDFFLGGRAS	234	Qy 64684	PRELIMINARY;
Db	132	ELITEHRRRLAETITEMIHAASLHDDVIDDDESMDNRGREYHELFGTRYAVLAGDFMFQAWS	191	ID Q64684;	PRT;
Qy	235	VALARLRNPVEVILLATVANLYVEGEFMQLKNTVDAALEATATQETPDYLYOKTYLTAS	294	AC Q64684;	297 AA.
Db	192	WYLANLENLEVKLISIVKDFASGE1KQASSIFD-----CDTKLDEYLJKSFYKTAS	244	DT 01-AUG-1998 (TREMBLrel. 07, Created)	
Qy	295	LIASKCRASALLGGATPEVADAYAYGRNLGAFOIQIVDDMLDYTVSATDLGKPGADQL	354	DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)	
Db	305	GINTATPVALERPRELIEREPRRELIIESEFCAGSLEEAIEVTKGSSGIKRAQELAREKADAI	364	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
Qy	415	AIRTFPESPARKALEQL	431	DE Putative trans-prenyltransferase.	
Db	365	NLQCLPSSGFRSALEM	381	AT2G34630.	

GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

Run on: January 16, 2003, 06:38:46 ; Search time 2939 Seconds
(without alignments)
16368.472 Million cell updates/sec

Title: US-09-830-111A-1

Perfect score: 1653

Sequence: 1 tttttgtgggtcgaaaaatgc.....atggcaactcaggaaatgaa 1653

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054610 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109260

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_Dh:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fuu:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_p1:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_Pln:*

35: em_htg_rdi:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query %	Match	Length	DB	ID	Description
	1	1653	100.0	1653	6	E51323		Process for Schizosaccharomyces pombe
	2	242.8	14.7	224	8	D84311		Mucor circinelloides
	3	231.4	14.0	2666	8	A7496300		GDNA endo
	4	222	13.4	1124	6	E13333		Schizosaccharomyces pombe
	5	218.6	13.2	1492	8	D89265		Allium sativum
	6	199.6	12.1	2097	8	SPB05694		U62637 Cloning vector
	7	198.6	12.0	5371	12	CYT062637		U62637 Cloning vector
	8	198	12.0	4176	6	A13038		Artificial M22744 Cloning vector
	9	198	12.0	4176	12	SYNTRC99A		U13872 PTrc99a clo
	10	198	12.0	4176	12	XXU13872		A59289 pSEC-Bp1 co
	11	198	12.0	4239	6	A29589		X81838 E.coli DNA
	12	197	11.9	4613	12	ASPBAD18		U02444 Cloning vector
	13	197	11.9	5075	12	U02444		AY075463 Drosophila melanogaster
	14	186.4	11.3	2199	3	AY075463		X81837 E.coli DNA
	15	186.2	11.3	4542	12	ASPBAD24		AY112733 Broad host range phage
	16	186.2	11.3	6775	12	AY112733		AF118855 Mus musculus
	17	185.6	11.2	1282	10	B026820		BC026820 Broad host range phage
	18	185.6	11.2	1552	10	BC026820		AY112734 Broad host range phage
	19	185.4	11.2	6124	12	AY112734		L24193 Cloning vector
	20	184	11.1	4232	12	SYNBLACQ		L24367 Cloning vector
	21	183	11.1	4735	12	SYNBETALAC		AJ29245 Quercus robur
	22	182.8	11.1	1600	8	QRO298245		Y17376 Arabidopsis thaliana
	23	182.4	11.0	1402	8	ATH17376		AJ093006 Arabidopsis thaliana
	24	182.4	11.0	1408	8	AY093006		AX043804 Sequence
	25	180.8	10.9	966	6	AX043804		AX428168 Sequence
	26	180.8	10.9	966	6	AX360800		X95387 Expression
	27	180.8	10.9	966	6	AX428168		AJ243739 Citrus sinensis
	28	180	10.9	4991	12	EUPK2333		A0357 Plasmid pIG
	29	179.8	10.9	1114	8	CSPPA43739		D13250 Plasmid pUT
	30	178	10.8	2681	12	SYNPUT18		AF118395 Homo sapiens
	31	171.8	10.4	1485	9	AF118395		AF005375 Thermosyne humilis
	32	171.8	10.4	298750	1	AK024802		AK024802 Homo sapiens
	33	168.6	10.2	1641	9	AK024802		AY027815 Sequence
	34	165	10.0	5241	6	AX027815		A0357 Plasmid pIG
	35	160.4	9.7	3302	6	A20358		A0355 Plasmid pIG
	36	160.4	9.7	3302	6	A20358		D90899 Synechocystis sp. PCC 7120
	37	159.6	9.7	133859	1	A39734		A009734 Sequence
	38	155.2	9.4	4009	6	A39734		AR069625 Sequence
	39	155.2	9.4	4009	6	A39734		A99078 Sequence
	40	152.4	9.2	3423	6	A39734		AR195392 Sequence
	41	152.4	9.2	4633	6	A20356		AR008977 Sequence
	42	152.4	9.2	4633	6	A20356		AR008977 Sequence
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ALIGNMENTS

RESULT	1	1653 bp	DNA	linear	PAT 31-JAN-2002
ES1323					
LOCUS					
DEFINITION					
ACCESSION					
	E51323				
		Process for producing coenzyme Q10.			
VERSION					
	B5123				
		GI:18633579			
SOURCE					
	JP 2001061478-A/1.				
ORGANISM					
	unidentified				
	unclassified				
REFERENCE	1 (bases 1 to 1653)				
AUTHORS	Matsuda,H., Kawamukai,M., Hasegawa,J., Ikenaka,A.,				
TITLE	Processes for producing coenzyme Q10				
JOURNAL	Patent: JP 2001061478-A 1 13-MAR-2001;				

	KANEKA CORP
COMMENT	
OS	Saiocella complicata
PN	JP 200106478-A/1
PD	13-MAR-2001
PF	24-AUG-1999 JP 1999237561
PR	
PI	HIDEYUKI MATSUDA, MAKOTO KAWAMUKAI, AKIYOSHI YAJIMA, PI
PI	YASUHIRO IKENAKA, JUNZO HASEGWA, SATOMI TAKAHASHI
PI	C12N15/09, C12N1/21, C12N9/12// (C12N1/21, C12R1:19), (C12N9/12, PC
PC	C12N15/00
CC	
PH	Key
FT	Location/Qualifiers
FT	source 1..1653 /organism="Saiocella complicata".
FEATURES	location/Qualifiers
source	1..1653 /organism="unidentified"
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Best Local Similarity	100.0%; Pred. No. 0;
Matches	1653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1 TTGTTGGGGTCGAAAGTCGGACGGGTGCAAGCTTGATGAGCTTGTGCTACTGAACTT 900
Qy	61 GAGATGGAGGTCAGGACAAAGCTTGATCGCTGAGGCTACACTTCAGCAAATCATTC 120
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Qy	121 AAATCCATATACCATGGCTCACCAGCAGCTGCGATAAGAACATCACCTCTGATCAT 180
Db	121 AAATCCATATACCATGGCTCACCAGCAGCTGCGATAAGAACATCACCTCTGATCAT 180
Qy	181 CGCTCTCTGCGATCGTTACCCCTACCGACCTTCAGCTAACAGACGCTCGGCCACT 240
Db	181 CGCTCTCTGCGATCGTTACCCCTACCGACCTTCAGCTAACAGACGCTCGGCCACT 240
Qy	241 TACCCCGAGGAGCGGGCTCTGAGTTACCCCTACCGACCTTCAGCTAACAGACGCTCGGCCACT 300
Db	241 TACCCCGAGGAGCGGGCTCTGAGTTACCCCTACCGACCTTCAGCTAACAGACGCTCGGCCACT 300
Qy	301 GGTGAGCTGATCGGAATCAACTCTCTCATCACTCGCTCAACTTGTGGTCCGGAGAT 360
Db	301 GGTGAGCTGATCGGAATCAACTCTCTCATCACTCGCTCAACTTGTGGTCCGGAGAT 360
Qy	361 GTCAAATCTACATCCAAATCCAGATCTCTCTCGGTGTTAGGACACCTCTCGAGAC 420
Db	361 GTCAAATCTACATCCAAATCCAGATCTCTCGGTGTTAGGACACCTCTCGAGAC 420
Qy	421 TGTGCTCTAAATCATGTTAGTGTAGCTGAGGGAACGATATTCGTCGCTCATGGTACTGT 480
Db	421 TGTGCTCTAAATCATGTTAGTGTAGCTGAGGGAACGATATTCGTCGCTCATGGTACTGT 480
Qy	481 GATGGCTCGGGACGGAGTTGGCCAAAGTCAGCTTGGAGAAGGTCTGGAGGT 540
Db	481 GATGGCTCGGGACGGAGTTGGCCAAAGTCAGCTTGGAGAAGGTCTGGAGGT 540
Qy	601 GAACTGAGGACTCTGCCACCAACCAAGGAGTCAGTGAAGACCCAGATATGT 600
Db	601 GAACTGAGGACTCTGCCACCAACCAAGGAGTCAGTGAAGACCCAGATATGT 600
Qy	661 CCTGGCTCGCAACGGCGCTTGCTGAGGTACCGGAGTCAATGACAGAACCCAGATATGT 720
RESULT	2
D84311	Locus D84311
DEFINITION	Schizosaccharomyces pombe gene for decaprenyl diphosphate synthase, complete cds.
ACCESSION	D84311

VERSION	D84311.1	GI:1845554	Query Match	Qy	1009	TGCGTCCCTGTATTGCCAAGTCGCTGCAGAGCAAGTGCCCTTCGGGTGTTGCTACGGCTGA 1068
KEYWORDS	dps; decaprenyl diphosphate synthase; ubiquinone biosynthesis.			Db	1036	AGCCAGTTTAATTCCAAAGTGCAGGCTTACATCCTCGAACATGTTCTCAC 1095
SOURCE	Schizosaccharomyces pombe			Qy	1069	GTTGCTGTGCTGCTTATGCTTACGGAAAGAACCTGGTTGGCATTCGATCGCTGA 1128
ORGANISM	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyces pombe			Db	1096	TCTAGAACAGCTGGAGATACTGGATCTTCAACTAATGGA 1155
REFERENCE	1 ("sites")			Qy	1129	CGACATGCTGCTGCTACCGCTTCGGTACCGACCTCGTAAGCCCCGGTGCAGACT 1188
AUTHORS	Suzuki, K., Okada, K., Kamiya, Y., Zhu, X. F., Nakagawa, T., Kawamura, M., and Matsuda, H.			Db	1156	TGACGTGTTGGACTATACTGTCGAAAGATGATACTTGTAGAAAGGGCTGGTCAGATT 1215
TITLE	Analysis of the decaprenyl diphosphate synthase (dps) gene in fission yeast suggests a role of ubiquinone as an antioxidant			Qy	1189	CGAGCTGGTCGCAACGCCGGCCTCTCGATGGAGCACCAAGCGGAGTCGG 1248
JOURNAL	J. Biochem. 121 (3), 496-505 (1997)			Db	1216	GAAGCTTGGGTGGCTAGTCGGTCCGTCCTTGTGATGGAAAAGTTCGAACTGG 1275
MEDLINE	97279041			Qy	1249	TCCCATGATCAAGGCCAGTTCCTGACCCAGGAGGTGGCCAGAGTCAGCGGAGTTGTT 1308
REFERENCE	2 (bases 1 to 2214)			Db	1276	TGCAATATTGGAATAGATTCATCCCTCTGTATCACCGCTCGTCTTGT 1335
AUTHORS	Suzuki, K.			Qy	1309	CGAGAAAAGTGTGGATTGGAAAGAGGAGGCCCTGGGAGGATATGGCCAGAGGC 1368
TITLE	Direct Submission			Db	1336	TGATGCGCACTGTGCTATGCAAAACATCAGTGGAAAGATAATATCAAAAGGC 1395
JOURNAL	Submitted (03-APR-1996) Kengo Suzuki, Shimane University, Faculty of Life and Environmental Sciences, Nishikawara 1060, Matsue, Shimane 690, Japan (E-mail: kawamura@botan.shimane-u.ac.jp, Tel: 0852-32-6587, Fax: 0852-32-6587).			Qy	1369	GTGGGAACTTCGAGGTTCCGGAGAGTCGGCAGGAGCTTGAGCGATGAC 1428
COMMENT	On Feb 21, 1997 this sequence version replaced gi:1304267.			Db	1396	CGAACAGTCCCTCTGTCCTGATTCACCTGCAAGGCACTTTGGGTGGC 1455
SEQUENCE	Sequence updated (19-Feb-1997) by:kengo Suzuki.			Qy	1429	GGACAAGGTGGTGAATG 1446
LOCATION/QUALIFIERS				Db	1456	TGATAAACATAAACGAG 1473
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SOURCE				MC1496300		
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CDS	/db_xref="taxon:4896"			DEFINITION	Mucor circinelloides f. solanius isOB gene for solanesyl pyrophosphate synthase	linear
gene	/db_xref="dps"			ACCESSION	AJ496300	exons 1-3.
	347 .. 1483			VERSION	GI:2195561	
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	/db_xref="GI:1845555"			AUTHORS	Velayo, A.	
	/translation="MIOYVYKXHMRKWLISLGKVRSTVLRFSTINRNASHLIIKNELEQI			TITLE	Carotenogenesis en Mucor circinelloides	
	SGDILRNLNSBFLBECISKYTIACQPSLVLMSKPSLCHGIDRRAVGDKYI			JOURNAL	Thesis (2001) Departamento de Microbiologia y Genetica, Universidad de Salamanca, Salamanca, Spain	
	DDDLRSFSTGOLPSQRLAQTTCAGTAAITMHNIAQHDDVIDHANVRERSPSNVAFNRR			REFERENCE	2	
	SILAGNPILARASTAMARLNPOVTELLATIADLVGEFTQLKNTMDPSSLEIKOSN			AUTHORS	Prenyl synthases in Mucor circinelloides	
	SKDTDTLKAAGADLKLUGLTAAPFLAWKKYELBGLANTVNRLNHPSPDIQRARSVLECTD			JOURNAL	Unpublished (22-JUL-2002) Velayos A., Aguilar,R., Eslava,A.P. and Iturriaga,E.A.	
	ALEQITWAKSYKIKKADSLLCLPDSPARKALFALLDKVTRKK"			REFERENCE	3 (bases 1 to 2666)	
BASE COUNT	676 a 408 c 403 g 727 t			AUTHORS	Velayo, A.	
ORIGIN				TITLE	Direct Submission	
				JOURNAL	Submitted (22-JUL-2002) Velayos A., Microbiología y Genética, Área Genética, Facultad de Biología, Universidad de Salamanca, Edificio Departamental, Avenida del Campo Charro s/n, Salamanca, E-37007, SPAIN	
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					/codon_start=1	

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EKRHGLMSFKSTVLGSPPLRNTTKPVIPFTGEANNNQALSEAQSIVKDSDDRID	EMITIASLHADDIDASMRMRRNNEASAFGNKAVALGGDFLIARASLAIRANAE	Db	1401	GAACACCAACAGGGAGATCGGGCAAGGTGAAAGACCTTGACCATTAACATCA	1460
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LFWAKYEPLEPLKRSVKGDEEKARDLVQSGDUKKTLDIQLHQCKLTDALYKL	PASARSALVVOITKLUTRS"	Db	1461	TGGAGAAGACCTACATGAGAGATCGGCACTCTATGCCAGAGCACCTG	1520
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exon	/gene="isoB"	Db	1581	GTCTAGCCCTTCAGTAATACAAAGGAAATCTTATCACCCCTGTAACACTCTTC	1640
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Best Local Similarity	54.6%	Pred.	No. 1.9e-39;	Mismatches	396; Indels 67; Gaps 2;
Matches	556;	Conservative	0;	Number	1.9e-39;
Qy	327	TCATCAATCGCTCACTTGCTGGTCCAGAGATCTCAATCTAACATCCGAT	386		
Db	813	TAATTGATCTCTGCCAACACTAGTGGAGACATCTCAAAGAACATCTCCA	872		
Qy	387	CTCTCTCGCTTCAGACACCCCTCTCGACACTGCTGCTAAATACTATGTCGTC	446		
Db	873	AATTGCTGGCGCAGTGACACCGTCTCAACACCGTGGCCAGACTACTTACGGGG	932		
Qy	447	AGGGAAAGATACTGTCCTCATGGTACTCTGCTGATGGCTCAGCGAGGAGTTGCG	506		
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Qy	507	CAAAAGTTCAAGGTTGGAGAAGGTGTTGGAGGTTCCGGTAAGCGAGGACTCGGACCA	566		
Db	993	ACAAA-----AACTCGTTGGCCAGCAACATGACTACAAATCGATCGCACAC	1040		
Qy	567	CAGAGGTGCTCAATGACAAGAACCGAGATATGATCACATGAGGTCAAGGACATTACGA	626	RESULT 4	
Db	1041	CTATATCGCATGAGCTCAAGACATACCAACCAAGACGCTGTTGACCGAAGCTTACAT	1100	LOCUS	E13333
Qy	627	AGGAGCGGAGATCCAGGGAGAGCGAGCTGATACTCTCGCTCCAAAGCGGTTGGCTG	686	DEFINITION	gDNA encoding prenyl diphosphate synthase.
Db	1101	ACACACCCCTCGTGHAGATCAGCGATCATCTTACCCACAGCAGCTTACAGCAGATTTAGCAG	1160	ACCESSION	E13333
Qy	687	AGATCAGCGAGATGATGCCATGAGATCACTCCACAGAGCTTATGACCGGTTCCG	746	VERSION	E13333.1
Db	1161	AAATTCGGAGATGATCATACGGGCTTACATACAGTGTAGTGTAGCTGACCCCTCGA	1220	KEYWORDS	JP 1997173076-A/1.
Qy	747	AGACCGAGACAAACCAACCATCCGAAACAGGCTTCGAAACAGATGGCTATTGCG	806	SOURCE	Schizosaccharomyces pombe.
Db	1221	TGACTCGCAGAAACTGCGTCCGCAATGCGCTCTTGGCAACAAATGGCAGGTGCTGG	1280	ORGANISM	Schizosaccharomyces pombe.
Qy	807	CTGGTATTCCTGTTGGAGGGCTCTTGGCTTGGAGGTGGCAATCGGAGG	866	REFERENCE	Bukar-Yata, Fungi; Ascomycota; Schizosaccharomycetes;
Db	1281	GCggGGACTCTCTGGCCAGAGCATCATGGCTTGGCAAGAACCTGCAAAACGCGAGT	1340	AUTHORS	Schizosaccharomyces pombe.
FEATURES	source	COMMENT	1 (bases 1 to 1134)	JOURNAL	Matsuda, H., Kawamuki, M. and Nakagawa, T.
				PATENT	PROTECTION OF DIFFERENT KIND UNQUOTE
				OS	PATENT: JP 1997173076-A 1-08-JUL-1997;
				ALPHA- SHOKOHIN KK	ALPHA- SHOKOHIN KK
				PN	Schizosaccharomyces pombe
				PD	JP 1997173076-A/1
				PD	08-JUL-1997
				PI	27-DEC-1995 JP 1995351243
				PC	MATSUDA, HIBIYUKI, KAWAMUKI, MAKOTO, NAKAGAWA, TSUYOSHI
				PC	C12N15/09, C12N9/10, C12P7/66, (C12N15/09, C12R1:19), (C12N15/09, PC
				PC	C12R1:645), (C12N9/10, C12R1:865);
				CC	strandedness: Double;
				CC	topology: Linear;
				CC	hypothetical: No;
				CC	anti-sense: No;
				FH	Key
				FT	source
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				FT	/organism="Schizosaccharomyces pombe" /db_xref="taxon:4896"

RESULT 7
 CVU62637 LOCUS 5371 bp DNA linear STN 14-AUG-1996
 DEFINITION Cloning vector pBAD-GFPuv, complete sequence.
 ACCESSION U62637
 VERSION 1
 KEYWORDS GI:1490531
 SOURCE Cloning vector pBAD-GFPuv.
 ORGANISM Cloning vector pBAD-GFPuv
 ARTIFICIAL SEQUENCES; VECTORS.
 REFERENCE 1 (bases 1 to 5371)
 AUTHORS Cramer, A., Whitehorn, E.A., Tate, E. and Stemmer, W.P.
 TITLE Improved green fluorescent protein by molecular evolution using DNA shuffling
 JOURNAL Nat. Biotechnol. 14 (3), 315-319 (1996)
 MEDLINE 98293348
 PUBMED 9630892
 REFERENCE 2 (bases 1 to 5371)
 AUTHORS Cramer, A. and Kitts, P.A.
 TITLE pBAD-GFPuv complete sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 5371)
 AUTHORS Kitts, P.A.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1996) CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303-4230, USA
 COMMENT This vector can be obtained from CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303-4230, USA. To place an order call (415) 421-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH. If you suspect there is an error in this sequence, Please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES

Source	Organism="Cloning vector pBAD-GFPuv"
	/db_xref="Taxon:50707" complement(96..974)
gene	/Gene="araC" Complement(96..974)
CDS	/note="PID: g455167" /codon_start=1

RESULTS

8	A13038
LOCUS	A13038
DEFINITION Artificial sequence of plasmid pTrec9A.	A13038
ACCESSION	A13038
VERSION	A13038.1
KEYWORDS	GI:491502

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 YWHEWNPWSIFANTCFFRPDAHQPHPSLAFQDLSNFIASVQHVLSPSRSLHFLFQ
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 RAGCEBETVNDYAVKL\$"
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 CDS 1342 .. 2061
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 BIGASLKHW"
 ORIGIN BASE COUNT 1369 a 1368 c 1300 g 1334 t
 Query Match Score 198.6; DB 12; Length 5371;
 Best Local Similarity 98.0%; Pred. No. 2, 2e-32;
 Matches 201; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1449 CAAGATAGGAATTGAGCTCGTAGCTAGTCGACCTGGGATCCCTAGACTCGCAGGGCATGCA 1508
 Db 2055 CAAATAATGAAATTGAGCTCGTAGCTAGTCGACCTGGGATCCCTAGACTCGCAGGGCATGCA 2114
 Qy 1509 AGCTTGCGCTGTGTTGGCGATGAGAGATTTGGCTGATACGATTAATTCGAC 1568
 Db 2115 AGCTTGCGCTGTGTTGGCGATGAGAGATTTGGCTGATACGATTAATTCGAC 2174
 Qy 1569 GGAAAGCGGTGTGATAAACGAAATTGCGCTGCACAGTAGGGCTGTTGGTCCCACCTG 1628
 Db 2175 GGAAAGCGGTGTGATAAACGAAATTGCGCTGCACAGTAGGGCTGTTGGTCCCACCTG 2234
 Qy 1629 ACCCCATGCCGAACTCAGAACTGAA 1653
 Db 2235 ACCCCATGCCGAACTCAGAACTGAA 2259

2579077	4 (bases 328 to 753) Brosius, J., Dull, T.J., Sleeter,D.D. and Noller,H.F. Gene organization and primary structure of a ribosomal RNA operon from Escherichia coli	CDS /product=lacI /organism="Escherichia coli" /db_xref="GI : 555784" /transl_table=11	
2579078	5 (bases 1 to 4176) Malone, J.A. Direct Submission Dated: 19-AUG-1994; James A. Malone, International Technical Services, Molecular Biology Regents Division, Pharmacia Biotech Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA Location/Qualifiers	/product=lacI repressor protein /protein_id="AAAS6744.1" /translation="MKPVTYDVAEYAGVSQTVSRVNNQASHVSAXTRKEVAAAM LNYIPNRVAGQOLAGOSLLGIVATPSQLAIIAPSQIVAAIKSRAODLGASVYVSMVERS GVEACKAAAVNLIAQRVSGILLNYPILDQDAIAVEACTVNPALFLVSDQTPIINSI FWSHEGTRLVEHLYALGHQDIIAGPLSSVSARLQAGHKLTRNQIOPTAQER DWSAMSGFOQTQMOMNEGIVTAMLYVANDOMALGAMRATIESTSLRVGQDITSYVGDDT EDSSCYIPPLTIKODFRLLQTSVDRLLQLSOGQAVKGNOQLPVLVRKRTLAPNT QTASRALASLMLQARQVSRLSEGO"	
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2579080	193 - 222 /note="The trc promoter combines the -35 region from the trc promoter and the -10 region from the lacUV5 promoter" /citation=[3]	Qy 1456 CGAACATTGGCTCGGTACCCGGATCCTTAGAGTCACCTGCAGGATGCAAGCTGG 1515 Db 269 GGAATTGAGCTGGTACCCGGATCCTTAGAGTCACCTGCAGGATGCAAGCTGG 328 Qy 1516 CTGTGTTTGCCGATGAGAAGATTTTCAGGCTGTATAACAGATAAATCAGAACGCCAGAG 1575 Db 329 CTGTTTGGCCGATGAGAAGATTTTCAGGCTGTATAACAGATAAATCAGAACGCCAGAG 388	
2579081	193 - 198 /gene="trc"	Qy 1576 CGGTCTGATAAAACAGAAATTGGCTGGCAGTAGCTGGCTTACCTGACCCAT 1635 Db 389 CGGTCTGATAAAACAGAAATTGGCTGGCAGTAGCTGGCTTACCTGACCCAT 448	
2579082	193 - 198 /gene="trc"	Qy 1636 GCGGAACCTAGAAAGTGA 1653 Db 449 GCGAACTCAGAACTGAA 466	
2579083	216 - 222 /gene="lacUV5"	RESULT 11 A29289 LOCUS A29289 4239 bp DNA sequence from patent DE3901681. DEFINITION pSEC-Bp1 complete DNA sequence ACCESSION A29289 VERSION A29289.1 GI:1248952 KEYWORDS synthetic construct, synthetic construct, artificial sequences. ORGANISM FEATURES Location/Qualifiers source 1..4239 /organism="synthetic construct" /db_xref="taxon:32650" ORIGIN BASE COUNT 1019 a 1080 c 1137 g 1003 t	
2579084	228 - 248 /bound moiety="lacIq repressor protein"	Query Match 12.0%; Score 198; DB 6; Length 4239; Best Local Similarity 100.0%; Pred. No. 3e-32; Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
2579085	265 - 314 /note="Multiple Cloning Site (MCS); contains unique sites for NcoI, EcoRI, SacI, KpnI, SmaI, BamHI, XbaI, SalI, PstI, and HindIII"	Qy 1456 CGAACATTGGCTCGGTACCCGGATCCTTAGAGTCACCTGCAGGATGCAAGCTGG 1515 Db 332 GGAATTGAGCTGGTACCCGGATCCTTAGAGTCACCTGCAGGATGCAAGCTGG 391	
2579086	328 - 753 /note="derived from the rrnB operon; the entire operon is not contained in this vector"	Qy 1516 CTGTGTTTGCCGATGAGAAGATTTCAAGCTGTATAACAGATAAATCAGAACGCCAGAG 1575 Db 392 CTGTTTGGCCGATGAGAAGATTTCAAGCTGTATAACAGATAAATCAGAACGCCAGAG 451	
2579087	409 - 734 /gene="rrnB"	Qy 1576 CGGTCTGATAAAACAGAAATTGGCTGGCAGTAGCTGGCTTACCTGACCCAT 1635 Db 452 CGGTCTGATAAAACAGAAATTGGCTGGCAGTAGCTGGCTTACCTGACCCAT 511	
2579088	409 - 528 /gene="rrnB"	gene promoter terminator terminator gene promoter CDS	/product="rrnB" /product="5S ribosomal RNA" /standard_name="rrnB_T1" /standard_name="rrnB_T2" /standard_name="rrnB_T2" /gene="rrnB" /product="beta-lactamase" /product="beta-lactamase" /protein_id="AAAS6743.1" /db_xref="GI: 95783" /translation="MSIOTHRVALIIPFAAFCLPVPFAHPETLVKVRDAEDOLGARYGV IELDLNSCKLIESFRPERPFPMSTEKVLLCAVLSRDAGQEQLGRIRHYSONDLVE YSPFLCRLTDGIVRELLTIGGELTAFHNMGDHVTRL DRWEPELINEAIPNDNERDTTMTAMATTLRKLJTGELTILASRQOLIDMEADYKAVGPL LRSALPAGWFIADKSGAGERGSRGIIIAALGPDCPKPSRIVVITYGSQATMDERNRQIA EIGASLKHWW" rep_origin /note="base 2464 represents the first base of the newly synthesized single strand" /direction=-right gene

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DEFINITION E.coli DNA for pBAD18 cloning vector.
ACCESSION X81838
VERSION X81838.1 GI:51423
KEYWORDS arac gene; bla gene; expression vector;
synthetic construct;
artificial sequences.
REFERENCE 1 (bases 1 to 4613)
AUTHORS Guzman,L.M.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1994) L.M. Guzman, Harvard Medical School, Dept
of Microbiology & Molecular Genet., 200 Longwood Ave., Boston, MA
02115, USA
2 (bases 1 to 4613)
Guzman,L.M., Belin,M.J. and Beckwith,J.
Tight regulation, modulation, and high-level expression by vectors
containing the arabinose PBAD promoter
J. Bacteriol. 177 (14), 4121-4130 (1995)
MEDLINE 9533220
PUBMED 7650887
COMMENT Related sequences: J01641 and M10196 (bases 1-1300); M77749 (bases
1357-2296; 4537-4613); SYNPBR322 (bases 2297-2780); Gene 27, 183,
1984 (bases 2780-3218).
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Matches 0;
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Db 1306 GAATTGGAGCTTGATCCGGGTACCTGAGTCAGCTGAGCTGGC 1516
QY 1517 TGTTTGGCGTAGAGATTTCAGCTGATACAGATAATCAGAACCGAGGC 1576
Db 1366 TGTTTGGCGATGAGAGATTTCAGCTGATACAGATAATCAGAACCGAGGC 1425
QY 1577 GGTCGATACAGAATTTCGGCGCATGAGCGGGTGTCCACCTGACCCATG 1636
Db 1426 GGTCGATACAGAATTTCGGCGCATGAGCGGGTGTCCACCTGACCCATG 1485
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Db 1486 CGGAACCTCAGAGTGA 1502

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Matches 0;
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Db 309 TATGATATGGAGGTTAACCTGGAGCTGAATCGAGCGGGTACCCGGGATCT 368
QY 1485 CTAGAGTCGACTCTGAGGATGCAAGCTGCTTGTGGGATGAGAGATTTCA 1544
Db 369 CTAGAGTCGACTCTGAGGATGCAAGCTGCTTGTGGGATGAGAGATTTCA 426

TITLE Direct Submission
JOURNAL Submitted (22-SEP-1994) L.M. Guzman, Harvard Medical School, Dept
of Microbiology & Molecular Genet., 200 Longwood Ave., Boston MA
REFERENCE 0215 USA
2 (bases 1 to 4542)
AUTHORS Guzman,L.M., Belin,D., Carron,M.J. and Beckwith,J.
TITLE Tight regulation, modulation, and high-level expression by vectors
containing the arabinose PBAD promoter
JOURNAL J. Bacteriol. 177 (14), 4121-4130 (1995)
MEDLINE 95332220
PUBMED 7608087
COMMENT Related sequences: J01641 and M0196 (bases 1-1300); M77749 (bases
1366-2300; 3242-4542); Gene 33, 103, 1985 (bases 2300-2784); Gene
27, 183, 1984 (bases 2784-3242).
FEATURES LocationQualifiers
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/misc_feature 1204. .1217
/note="CAP site"
/misc_feature 1213. .1251
/promoter 1250. .1277
/note="PBAD promoter"
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/RBS 1306. .1311
/note="multiple cloning site"
/misc_feature 1317. .1318
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/db_xref="G1:55145"
/translation="MVPGDPLESTCRHASLAVLADERRFSA"
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/gene="rrnB P3 promoter"
1885. .2748
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1885. .2748
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rep_origin 2784. .3242
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3248. .3945
/note="pBR322 origin"
BASE COUNT 1110 a 1191 c 1136 g 1105 t
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Best Local Similarity 91.6%; Pred. No. 1e-29; Gaps 0;
Matches 197; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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Db 1292 TTTTTGGCTAGCAGGAGAATTCACCATGTTACCCGGGATCCTCTAGAGTCGACCTG 1351

Search completed: January 16, 2003, 08:18:44
Job time : 2967 secs

QY 1499 CAGGCATGCAAGCTTGGCTGTTGGCGATGAGAGAGATTTCACCTGTACAGATT 1558
Db 1352 CAGGCATGCAAGCTTGGCTGTTGGCGATGAGAGATTTCACCTGTACAGATT 1411
QY 1559 AAATCAGAACGAGAAAGGGTCTGATAAACGAACTGCGCTGGCGAGGTTACGCTG 1618
Db 1412 AACTCAGAACGAGAAAGGGTCTGATAAACGAACTGCGCTGGCGAGGTTACGCTG 1471
QY 1619 GTGCCACCTGACCCATGCCGAACTCGAAGTGAA 1653
Db 1472 GTCCCCACTGACCCATGCCGAACTCGAAGTGAA 1506

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	KW	593	CGGATGATCCATACCGCTCTCGTCATGACGACTGACAGCTGTTACTC 652
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	PH		
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FT	/partial		
FT	/note="CDS lacks a stop codon"		
PN	WO20252017-A1.		
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XX	04-JUL-2002.		
PD			
XX	27-DEC-2001; 2001WO-JP11523.		
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PF	27-DEC-2000; 2000JP-039858.		
XX			
PA	(KANP) KANEKA CORP.		
XX			
PI	Matsuda H, Kawamukai M, Yajima K, Ikenaka Y;		
XX			
DR	WPI; 2002-500767/53.		
XX			
DR	P-PSDB; ABB83733.		
XX			
PT	Microbial production of coenzyme Q10 by transformants transferred with		
PT	fungal decaprenyl diphosphate synthase gene, on industrial scale for		
PT	application in drugs -		
PT	Claim 2; Page 29-33; 52PP; Japanese.		
PS			
XX	The invention relates to a DNA sequence (I, ABN81604-ABN81605),		
CC	containing a sequence based on that of (I) but with some bases deleted,		
CC	added, inserted and/or substituted and encoding a protein		
CC	(ABB83792-ABB83793) with decaprenyl diphosphate synthase activity or		
CC	hybridisable with (I) under stringent conditions and encoding a protein		
CC	with decaprenyl diphosphate synthase activity. The DNA is useful for the		
CC	production of coenzyme Q10 for application in drugs. The coenzyme is		
CC	simply produced on industrial scale, efficiently, with significantly		
CC	productivity.		
XX	Sequence 1353 BP; 300 A; 396 C; 370 G; 287 T; 0 other;		
SQ	Query Match Score 395.8; DB 24; Length 1353;		
	Best Local Similarity 23.0%; Pred. No. 8.4e-92;		
	Matches 674; Conservative 0; Mismatches 442; Indels 3; Gaps 1;		
QY	333 ATCCGCTCACTTGTTGGTCCCAGATGTCAAACTTACATCCAAACATCGATCTCTCC 392		
Db	236 ATCCATTGAGATCGGGCAAAGCTCAAGTTTGTACGAAGATAATAGCCAAATTCGC 295		
QY	393 TCGGTTCAGACACCCCTCTCGAAGACTGTGCTAAATFACTGTTCACTCTGAGGAA 452		
Db	296 TGGGTTCGGCCACCCGACTTGTATAAATGGCCAAATTTACCCGGAGGGCA 355		
QY	453 AGCATATTGGCTCGCTCATGTTACTGTGCTGGCTCAGGGCAGGGTTGCCAAAAG 512		
Db	356 AACATATGGCTCGTGTGTTGTCCTGTCATGTCAGGGGACGGAGGTTCAGGGAA 415		
QY	513 TTCAAGGTTCGGAGAAGGCTGTGGAGGGTTCGGTAACGGGGACTCGC2CCACAGG 572		
Db	416 AGAGTCTGTTCAAACCTCACCCCTTCACAGTGTGTCATGTCCCCATTAGCTCGC 475		
QY	573 TGCTTAATGAAAGACCCAGATGACATAGTGAAGATAGGACCAATTACGAGGAGC 632		
Db	476 TCCTCGCGATAGAACCCGATTCAGAACCGATTCAGCCGCTGTGTCAGGAAAGCC 535		
QY	633 GCGAGATCAGGGACAGACCTGCAAAATCCCTGCCCTGCAACGGGGTTGCTGAGATCA 692		
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		ID AAL40138 standard; DNA; 1137 BP.	
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		DT	
		DE Isoprenoid related nucleic acid sequence SEQ ID No 43.	
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		KW Isoquinolin-1-deoxyxylulose-5-phosphate synthase; DXS; DDS;	
		XX	
		KW decaprenyl diphosphate synthase; ds.	
		XX	Schizosaccharomyces pombe.
		OS	
		XX	WO20226933-A2.
		PN	
		XX	04-APR-2002.
		PD	
		PP	28-SEP-2001; 2001WO-US30328.

Page 4

XX PR
XX XX
PA (CRGI) CARGILL INC.
XX PI
XX XX
DR XX
PT Substantially pure polypeptides having e.g., useful for the
PT 1-deoxyxylulose-5-phosphate synthase activity, useful for the
PT production of isoprenoids, especially CoQ(10)
XX PS Disclosure; Fig 13; 246pp; English.
XX CC The invention relates to methods and materials for the production of
CC isoprenoids. More particularly the invention provides isolated nucleic
CC acids, substantially pure polypeptides, host cells, and methods for
CC producing various isoprenoid compounds. The polypeptides are useful for
CC the production of isoprenoids, especially CoQ(10). Expressing the pure
CC polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS)
CC activity or deacetyl diphosphate synthase (DDS) activity, is useful for
CC increasing production of CoQ(10) in a cell having endogenous DDS
CC activity. This polynucleotide represents a nucleic acid sequence relating
CC to the isoprenoid production of the invention.
XX Sequence 1137 BP; 332 A; 220 C; 242 G; 343 T; 0 other;
SQ

The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ10. Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity or decaprenyl diphosphate synthase (DDS) activity, is useful for increasing levels of CoQ(10) in a cell having endogenous DDS activity. This polynucleotide represents a nucleic acid sequence relating to the isoprenoid production of the invention.

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333 GACGGGTCAATTCTCTTCATGAGATTAGCACAAATAACCGGAGAAGATCCATAT 392

```

453	AAGCATGTTGCTTGTGATTCAGGTCAATCCCTTGCGGTAATTGAGCTTTCGACTGT	512
829	GCGCTCTGTTGATGGAGGTGCGCAATCCGGAGGTAAATGAGCTTTCGACTGT	888

513	GCTTCGACTGCTATGCCCGCCCTCGAAATTCCCAAGTTCACGGAGTTGTTAGCTTCACT	572
889	TATTCGAACTTGTTGAGGGAGAGTCATTCAGTTGAAATACTGTGTGATGCGAT	948

573 GATAGCAGACTTGGTCGAGGTGAGTTTGACGTTAAAGATACTATGGAACCTTCATC 632
 949 TGGGCTAAGGGCGCAGAAACCTTCGATTAATCTATTGCGAGAAGACTTCTTGAGAC 1008

1069 GGTGCTGATGCTGCTTACGGAAAGAACCTGGTTGGCATTCGAGATCGA 1128
.....
.....

QY	1189	CCAGCTCGGTCGCCAACCGGCCGCCCCCTCTCGATGGAGCACCAAGCGAGCTGG	1248
Db	870	GAAGCTAGTGTGGCTACAGTCCGTCCTTGTGAGAAAGATTAACAGAATTGG	929

Db	930	TGCCATGATGTGATAGATATTCACTCATCCTCTGATA-TCCAAAGGGCTCGTTTGGT	989
QY	1309	CGAGAAACGTGATGGAGAGACGGAGGCTTGCGGAGGATGCCCCGAAGC	1368
Db	990	TGAGTCAGTGTATGAGAACATCACTTGGGAAGATATATCAAAGC	1049
QY	1369	GTGAGATGGAAATTGGACTTCCGGAGGCTGGCAGCGAAGGCTTGAGGAGTGTGC	1428
Db	1050	CAAAAGATTCTCTCTGTGTCCTCGATTTACCTGCAAGGAAGCACTTTGGTGGC	1109
QY	1429	GGACAAGGTTGTAAG 1446	
Db	1110	TGATTAAGTATAACGAG 1127	
RESULT	4		
AAL42942			
ID	AAL42942	standard; DNA; 1212 BP.	
XX			
AC			
AA	AAL42942;		
XX			
DT	08-AUG-2002	(first entry)	
XX			
DE	Rhodotorula minuta decaprenyl diphosphate synthase 3 coding sequence.		
KW	Fungi; decaprenyl diphosphate synthase; gene; ds; enzyme;		
CC	fungi; decaprenyl diphosphate synthase; gene; ds; enzyme;		

Db	191 AGGCCAACATATTCGGCCPATGATCTGTTCTCATGTRCCAAAGCCAAACCGTCTAG	RESULT 6
Qy	506 CCAAAGTTCAAGGTCTAGGGTTGGGAGAAGGTCTGGAGGACTCGCACCA	AAL42940
Db	251 CGCCCCGGTTTGAAAGAACGCTCAAATTGAACTCATCAGTCGGAAACAGACTGATCC	ID AAL42940 standard; DNA; 1614 BP.
Qy	566 CCAG-----AGTGCTCAATGCAAGAACCGGATATGATORACATGGAGTAGGCAC	AC
Db	311 CCAGGTCATCAATGATCTCTGAGATGAGATCTCACAGATGATTCGAACT	XX
Qy	618 CATPACAGGAAGGAGG-----GCGAGATCGAGGACAGACGCTGAGATA	XX
Db	371 CCTCTGCTCTGCTGCTGCGAAGGGGGTTGGTGGAGATCACCGAGATGCTGAACT	DE
Qy	660 TCCCTGCTGCAAGGGGGCTCGCGCTGAGATGATCCGAGCATACTCC	Rhodotorula minuta decaprenyl diphosphate synthase 1 coding sequence.
Db	431 TCCPACCCCTGCAAGAACGACGCTCGGGAAATCACGAATGATCCACGATGCTGAT	XX
Qy	720 TCCACGACGAGCTTATCGACGCTTCGAGACGACCATCGGAAACCG 779	KW; decaprenyl diphosphate synthase; gene; ds; enzyme;
Db	491 TGCAGACGATGTCAAGCGATGAGGAGCACAGCGTCGGCGCTCG 550	KW high-yield fermentation; coenzyme Q10 production.
Qy	780 CATTGGAAACAAGTGGGATTTGGCTGTGATTCCTGTTGGACGGCGCTCG 839	OS
Db	551 CATTGGAAACAAGTCTCGGTGCTGGCGGGATTCCTGCTCGCTCGCTG 610	XX
Qy	840 CATTGGAGGTGGCAATCGGGGGTGTGATGAGCCTTGGCTACTGTATGAACT	PR
Db	611 ACCTCTCCGACTAGGGACACGAGGTCTCGAGCTAATGCTCCGCTGCTAATC	FT
Qy	900 TGGTGGAGGAGASTCTATGCACTGTTGAGAAAATACTGTGTGATGATCGATT	FT
Db	671 TAGTGAGGGCAACTCATGCGATCAAGGAATGCTCTGAAATGCAAGGGAA	FT
Qy	950 -----GAGGCTACGGGACGGAGAACGTTGATTAATTTGGAGA 995	Key
Db	731 GCAAAAGAGGTAGCAGTCACAGATGACAGATGACCCGGAAATTTCGAACATTATGAGAAGA	location/Qualifiers
Qy	996 CTTACTTGAAAGACTCGTCTGATGCAAGTCGAGCAGTCGTTGGGT	1.1614
Db	851 GAGCGGGAGAAAGAGGGGGATAGAGGGCGACGCATAAAACATGCTGTACTG	/tag= a
Qy	1092 ACGGAGGACCTGTTGCAATCCAGATCGTGAGCACATGCTGCACTCCGCT	/product = "Rhodotorula minuta decaprenyl diphosphate synthase 1"
Db	911 ACGGTGGCACTAGTATGCTTCCAGTCGTCGACGATCTAGATTACGCTA	synthase 1"
Qy	1152 CCGCTACCGACCTCGTAAGCCCG-----CGTGACCTCCAGTCGGCTCGCACCG	PR
Db	971 CAGAGCGCAATTCGCAAGCCCTACAGGGTGCGATCTGAACTGTCGGCTCCAACTG	CDS
Qy	1209 CGCCGCCCTTCATGCAAGGCCAACCCGACTCTGGCCCTGATCAAGCCAACT	WO200240682-A1.
Db	1031 CGCCGCCGCTGATCCGATGGGAAGGTCCGGAGATGGCAATCTCCGCAAT	XX
Qy	1269 TCTCGACCAGGAGACCTGAGCTGAGCTGAGGAGATGCTGAGATGCTGAGATGCTG	XX
Db	1091 TTGAGAACGAGGCCATGTCGAACCTGCGAGAACTGCGAACTGAGTCAGTCGACCG	XX
Qy	1329 AGAACGAGAGCCTGGGGAGGTATGCCAGAGGGTTGGATGCAATCGACGT	XX
Db	1151 AAAGAACCGCTGAATTTGGCGAAAMACATCCGCACTCGCAATGCGGCTGGGGAT	XX
Qy	1389 TCCCGAGACTCCSACGGAGGGTTGGAGCAGTGGGACAGGTTGACTAGT	XX
Db	1211 TGCCGAGACTCTAGAGAGGCTGAGGCTCGAGGCTGCTGACAAAGCTGCTCACCGAA	XX
Qy	1449 CAAGTAG 1456	Rhodotorula minuta.
Db	1271 CAAAGTAG 1278	
Qy	566 CCAG-----AGGTGCTCAATGACAAGAACCCAGATATGATGACATGAGCTCAGGAC	

PT economic large-scale fermentative production of proteins
 XX
 QY 1009 TCCGTCCTTGATGCCAAGTGTGGAGCAACTGGCGCTCTGGGGCTACCCCTGA 1068
 DB 687 ACACCCAGTTATTCTCAAAGCTGCAGGTTCTACAATCTCGACATGTTCTCTAG 746
 QY 1069 GGTGCTGATGCTGCTTAAGGAACTTGTGGATCAGATCGATCTGA 1128
 DB 747 TGTAGGAAACAGCTGCTGGGAATAGGGTGTATGATGATGTTCAACTATGGA 806
 QY 1129 CGACATGCTGACTCACCGTCTCGCTACGGCTCGAACGCTCGAGACCT 1188
 DB 807 TGACTGTTGACTATCTGAGAAGATACCTTAGGAAGGGCTGTGAGATT 866
 QY 1189 CCAGCTCGCTCTCCACCGGGGGCTCTTGATGAAAGCCAGCCAGCTGG 1248
 DB 867 GAAGCTTGGGTTGCTACAGTCCGCTCTTCATGGAAAGTATCCAGACTTGC 926
 QY 1249 TCCCATGATAAGGCAAGTCTGACCAAGGACGGTGGAGGGTGG 1308
 DB 927 TGCATGATGTTGATAGATTCATCATCCTCGATATCCAAAGGGTGTCTTGT 986
 QY 1309 CGACAAAGCTGATTGGAGAACGAGCAGAGCTGGGGAGGAGTATGCCAGAGC 1368
 DB 987 TGAGTGCATGATGATGAGAACACATCACITGGCAAAAGATAATCAAAGC 1046
 QY 1369 GTGGATGCAATTGGACGTTCCGGAGAGTCCGGACAGGAAGCTTGAGCGTTGAC 1428
 DB 1047 CAAAGATTCCTCTGTGTCTCCCTGATTCACTGCAAGAAGGCAATTGGTGGC 1106
 QY 1429 GGACAGGTTGAGTAG 1446
 DB 1107 TGATTAAGTATAACGG 1124
 RESULT 8
 ABAU4129
 ID ABAU4129 standard; DNA; 3753 BP.
 XX
 AC ABAU4129;
 XX
 DT 28-FEB-2002 (first entry)
 DE Plasmid PHCE19T(II) polynucleotide sequence SEQ ID NO:3.
 KW Promoter; gene expression; fermentation; D-AAT; Bacillus SK-1;
 KW D-amino acid aminotransferase; economic; large-scale protein production;
 KW circular; ds.
 OS Bacillus sp. SK-1.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT promoter 1..223
 FT /tag= "specifically claimed promoter region in
 FT Claim 1 (see ABAU4129)"
 PN WO200183787-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 26-APR-2001; 2001WO-JP03607.
 XX
 PR 27-APR-2000; 2000JP-0128528.
 XX
 PA (BIOLEADERS CORP.
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Sung M, Lee S, Hong S, Seo H;
 XX
 DR WPI; 2002-066535/09.
 XX
 PT Promoter sequence effective in Escherichia coli and Bacillus for

PT economic large-scale fermentative production of proteins
 XX
 QY 1009 TCCGTCCTTGATGCCAAGTGTGGAGCAACTGGCGCTCTGGGGCTACCCCTGA 1068
 DB 687 ACACCCAGTTATTCTCAAAGCTGCAGGTTCTACAATCTCGACATGTTCTCTAG 746
 CC The present invention describes a DNA sequence (I) comprising promoter activity in Escherichia coli or Bacillus cells, where the promoter is derived from the D-AAT (D-amino acid aminotransferase) gene of Bacillus SK-1. (I) can be used for the high level expression of a foreign gene in a bacterial host for economic and efficient large-scale production of proteins such as enzymes, cytokines and antibodies. The present sequence represents the plasmid PHCE19T(II) polynucleotide sequence comprising a specifically claimed promoter region from the present invention.
 XX Sequence 3753 BP; 953 A; 912 C; 929 G; 959 T; 0 other;
 XX Query Match 12.0%; Score 198; DB 24; Length 3753;
 XX Best Local Similarity 100.0%; Pedi. No. 9.4e-11; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 198; Conservative 0; Mismatches 0;
 DE 927 TGCATGATGTTGATAGATTCATCATCCTCGATATCCAAAGGGTGTCTTGT 986
 QY 1456 GGAATTGAGCTCGTACCCGGGATCCTAGCTGACCTGCAGGATGGAGCTGG 1515
 DB 226 GGATTCAGCTGGTACCCGGGATCCTCTGAGTCGACCTGCAGCATGCTGG 285
 QY 1516 CTGTTTGGCGGATGAGAGAATTCAGCTGAGATTAATCAGAACGAGAG 1575
 DB 286 CTGTTTGGCGGATGAGAGAATTCAGCTGAGATTAATCAGAACGAGAG 345
 QY 1576 CGGTCTGATAAACAGAATTCTGGGGCGTAGGGGGTCCACCTGACCCAT 1635
 DB 346 CGGTCTGATAAACAGAATTCTGGGGCGTAGGGGGTCCACCTGACCCAT 405
 QY 1636 CCCAACTCAGAATGAA 1653
 DB 406 GCGGAACTCAGAATGAA 423
 RESULT 9
 ABAU4130
 ID ABAU4130 standard; DNA; 3755 BP.
 XX
 AC ABAU4130;
 XX
 DE 28-FEB-2002 (first entry)
 KW Promoter; gene expression; fermentation; D-AAT; Bacillus SK-1;
 KW D-amino acid aminotransferase; economic; large-scale protein production;
 KW circular; ds.
 OS Bacillus sp. SK-1.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT promoter 1..225
 FT /tag= "specifically claimed promoter region in
 FT Claim 1 (see ABAU4129)"
 PN WO200183787-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 27-APR-2000; 2000JP-0128528.
 XX
 PR 26-APR-2001; 2001WO-JP03607.
 XX
 PA (BIOLEADERS CORP.
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Sung M, Lee S, Hong S, Seo H;
 XX
 DR WPI; 2002-066535/09.
 XX
 PT Promoter sequence effective in Escherichia coli and Bacillus for

X WPI; 2002-066535/09.

X Promoter sequence effective in Escherichia coli and Bacillus for
X economic large-scale fermentative production of proteins -
X Claim 7; Page 58-60; 65pp; Japanese.

C The present invention describes a DNA sequence (I) comprising promoter
C activity in Escherichia coli or Bacillus cells, where the Promoter is
C derived from the D-AAT (D-amino acid aminotransferase) gene of
C Bacillus SK-1. (I) can be used for the high level expression of a
C foreign gene in a bacterial host for economic and efficient large-scale
C production of proteins such as enzymes, cytokines and antibodies. The
C present sequence represents the plasmid pHCE19 (II) polynucleotide
C sequence comprising a specifically claimed promoter region from the
C present invention.

X Sequence 3755 BP; 951 A; 914 C; 932 G; 958 T; 0 other;

Query Match 12.0%; Score 198; DB 24; Length 3755;
Best Local Similarity 100.0%; Pred. No. 9.4e-41;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1456 GGAAATTCTGAGCTCGGTACCCGGATCCCTAGACTCGAACCTTG 1515
· 228 GGAAATTCTGAGCTCGGTACCCGGATCCCTAGACTCGAACCTTG 287

Y 1516 CTGTTTTGGGGATGAGAGATTTACGCCATGAGTCAACCTGACCTGG 1575
· 228 CGGTCTGATAAAAGATTCAGCTGGCATGAGCTTG 388

Y 1516 CTGTTTTGGGGATGAGAGATTTCAACCTGATACGATTAAATCGAACCGAG 1575
· 288 CTGTTTTGGGGATGAGAGATTTCAACCTGATACGATTAAATCGAACCGAG 347

Y 1576 CGGTCTGATAAAACAGAAATTGCTGGCATGAGATTTCAACCTGACCCAT 1635
· 348 CGGTCTGATAAAACAGAAATTGCTGGCATGAGATTTCAACCTGACCCAT 407

b 1636 GCCGAACCTGAGAATGAA 1653
408 GCCGAACCTGAGAATGAA 425

RESUME 10
D AAN0709 standard; DNA; 4176 BP.
X AAN0709;

X X 14-MAR-1992 (first entry)

E Sequence of plasmid pTrc99A contg. trc promoter, lacZ RBS, Nco I
E restriction site, polylinker and transcription terminator.

W High yield expression vector; E.coli vector; pTrc 89-1; placIQ;
W pBRJ22; ss.

N EP345615.A.
N 13-DEC-1989.
D 30-MAY-1989; 89EP-0109771.
R 08-JUN-1988; 88DE-3819463.
A (BEHW) BEHRINGWERKE AG.
I Amann E, Abel KJ;
R WPI; 1989 365408/50.

XX Plasmid pTrc99A contains the trc promoter from pTrc 89-1 (see
CC BP235978), the entire lacIQ allele from placIQ, a synthetic
CC oligomer providing an NcoI restriction site and a translation
CC initiation codon, a 55bp EcoRI-Hind III polylinker from pUC18, and a
CC transcription terminator from the rnb operon. The backbone is
CC PBR322 DNA, esp. having a deletion up to position 2066 to increase
CC the plasmid copy no.).

SQ Sequence 4176 BP; 1009 A; 1058 C; 1119 G; 990 T; 0 other;

Query Match 12.0%; Score 198; DB 10; Length 4176;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1456 GGAAATTCTGAGCTGGTACCCGGATCCCTAGACTCGAACCTTG 1515
Db 269 GGAAATTCTGAGCTGGTACCCGGATCCCTAGACTCGAACCTTG 328

Qy 1516 CTGTTTTGGGGATGAGAGATTTACGCCATGAGTCAACCTGACCTGG 1575
Db 329 CGGTCTGATAAAAGATTCAGCTGGCATGAGCTTG 388

Qy 1576 CGGTCTGATAAAAGATTCAGCTGGCATGAGCTTG 347

Db 389 CGGTCTGATAAAACAGAAATTGCTGGCATGAGCTTG 407

Qy 1636 GCCGAACCTGAGAATGAA 1653
Db 449 GCCGAACCTGAGAATGAA 466

RESULT 11
ID AAQ05397
XX AAQ05397 standard; DNA; 4189 BP.
AC AAQ05397;
XX DT 14-DEC-1990 (First entry)

XX Secretion Vector pSEC-BPI encoding Bordetella pertussis signal
DE sequence.

XX Secretion vector pSEC-BPI; Bordetella pertussis signal sequence;

XX Key
FT sig_peptide
FT /tag= ^a
FT note="from B.pertussis"
FT misc_RNA
FT /tag= ^b
FT misc_polylinker
FT /note="contains 11 restriction sites"
FT 405..407
FT /*tag= ^c
FT /label=stop codon
FT 42..426
FT /*tag= ^d
FT /label=stop codon
FT 43..436
FT /*tag= ^e
FT /label=stop codon
FT 216..221
FT /*tag= ^f
FT 192..198
FT /*tag= ^g

XX DE3901681-A.
XX DE3901681-A.
XX DE3901681-A.
PD 26-JUL-1990.
PF 21-JAN-1989.

Claim 6; Table, pages 6-8; 12pp; German.

XX PR 21-JAN-1989; 89DE-3901681.
 XX PA (BEHN) BEHRINGWERKE AG.
 XX PI Knapp S, Abel KJ;
 XX DR WPI; 1990-232260/31.
 XX DR P-PSDB; ARR96222.
 PT Signal peptide from *Bordetella pertussis* - causing secretion of heterologous proteins in *E.coli*, and expression vectors for isolating PT and testing signal sequences.
 XX PS Disclosure; spp; German.
 CC Complete sequence of pSEC-BP1. Constructed from a 3.1kb SacI-ScaI fragment of pRC9c-phoA-seq1 (including signal sequence) ligated to a 0.9kb SacI-ScaI fragment from pRC97A, DNA encoding an heterologous protein can be inserted into the polylinker region. Upstream of this is a strong promoter (perfect match to consensus -35 and -10 regions) and the B.pertussis signal sequence.
 CC Downstream are three stop codons, one in each possible reading frame.
 CC See also AAQ05398-005400 and AAQ05521-005526.
 XX Sequence 4189 BP; 1004 A; 1067 C; 1123 G; 995 T; 0 other;
 SQ Best Local Similarity 100.0%; Score 198; DB 11; Length 4189;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1456 GGAATTCGAGCTCGTACCGGGGATCCTAGACTGACCTGAGGGATGCACCTGG 1515
 Db 332 GGATTCGAGCTCGTACCGGGGATCCTAGACTGACCTGAGGGATGCACCTGG 391
 QY 1516 CTGTTTGGCGGATGAGAGATTTCAGCTGATACAGATAATCAGAACGGAGAG 1575
 Db 392 CTGTTTGGCGGATGAGAGATTTCAGCTGATACAGATAATCAGAACGGAGAG 451
 QY 1576 CGGTCTGATAAAACGAAATTGCTGGCGCAGTAGCGGGGTGGCCACCTGACCCAT 1635
 Db 452 CGGTCTGATAAAACGAAATTGCTGGCGCAGTAGCGGGGTGGCCACCTGACCCAT 511
 QY 1636 GCGGAACTCGAGGTGA 1653
 Db 512 GCGGAACTCGAGGTGA 529
 RESULT 12
 ABN84393 ABN84393 standard; DNA; 4665 BP.
 XX AC ABN84393;
 XX DT 01-OCT-2002 (first entry)
 DE Antibiotic-independent high expression vector phCB(III).
 XX KW Vector; phCB(III); glutamate racemase; enzyme; selectable marker; gene; ds.
 XX OS Chimeric - *Bacillus borstelensis*.
 XX OS Chimeric - Unidentified.
 PN WO200255716-A1.
 XX PD 18-JUL-2002.
 XX PP 11-JAN-2002; 2002WO-KR00048.
 XX PR 12-JAN-2001; 2001KR-0001690.
 XX
 PA (BIOL-) BIOLREADERS CORP.
 PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX Sung MH, Lee SG, Hong SP, Yoon EJ, Choi YH, Poo HR;
 XX PI 2002-557828/59.
 PT New antibiotic-independent plasmid vector, useful for stably expressing genes without the need for any antibiotic-resistant genes, and for producing other recombinant proteins or nucleic acids -
 XX PS Claim 8; Page 41-44; 45pp; English.
 CC The present sequence is that of novel antibiotic-independent high expression vector plasmid phCE(III), deposited in *Escherichia coli* as KCTC 0925 BP. The vector was constructed by insertion of the *Bacillus borstelensis* glutamate racemase (Glutu) gene (see ASN84392) into vector pHC89(III). The Glutu gene, being essential to the microbial survival, was utilised as selectable marker. A recombinant gene can be stably transcribed and highly expressed using this vector, without the use of antibiotic resistance genes. Production of GluRa from the vector is sufficient to provide D-glutamic acid for cell growth of a transformed host. The stability of the vector was confirmed using phCE(III)-TFL, which includes a tyrosine phenol lyase gene, by transfer to *E. coli* WM335 (a D-glutamate auxotroph) host cells and cultivation through 9 generations. When expression vector phCE(III)-TNA, which includes the Symbiobacterium tobiii SC1 trypophan indole lyase (TNA) gene, was transformed into *E. coli* WM335 and cultivated, TNA production increased with cell growth and a high expression level was maintained throughout the growth period. The TNA content reached about 40% of total cell protein. The vector resolves problems associated with the use of expansive inducers and antibiotic-resistance genes. It can be widely applied for large-scale production of exogenous proteins, with no adverse effect on the environment.
 XX Sequence 4665 BP; 1141 A; 1193 C; 1145 G; 1186 T; 0 other;
 SQ Best Local Similarity 100.0%; Score 198; DB 24; Length 4665;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1456 GAAATTCGAGCTCGTACCCGGGATCTCTAGTGACCTGACGCTTG 1515
 Db 226 GAATTCGAGCTCGTACCCGGGATCTCTAGTGACCTGACGCTTG 285
 QY 1516 CTGTTTGGCGGATGAGAGATTTCAGCTGATACAGATAATCAGAACGGAGAG 1575
 Db 286 CTGTTTGGCGGATGAGAGATTTCAGCTGATACAGATAATCAGAACGGAGAG 345
 QY 1576 CGGTCTGATAAAACGAAATTGCTGGCGCAGTAGCGGGGTGGCCACCTGACCCAT 1635
 Db 346 CGGTCTGATAAAACGAAATTGCTGGCGCAGTAGCGGGGTGGCCACCTGACCCAT 405
 QY 1636 GCGGAACTCGAGGTGA 1653
 Db 406 GCGGAACTCGAGGTGA 423
 RESULT 13
 ABN81604 ABBN81604 standard; DNA; 1506 BP.
 XX AC ABBN81604;
 XX DT 29-AUG-2002 (first entry)
 XX DE Fungal decaprenyl diphosphate synthase encoding DNA SEQ ID NO 1.
 XX KW Fungi; Aspergillus; Leucosporidium; coenzyme Q10; enzyme; decaprenyl diphosphate synthase; enzyme; gene; ds.
 XX OS Leucosporidium scotti.

CC cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL130511), expressed DNA sequences (AB101840-ABL16175) and the encoded proteins (ABBS7737-ABB2072).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 CC
 XX Sequence 1293 BP; 321 A; 375 C; 346 G; 251 T; 0 other;

Query Match 11.3%; Score 187.2; DB 23; Length 1293;

Best Local Similarity 54.1%; Pred. No. 4e-38; Matches 418; Conservative 0; Mismatches 333; Indels 21; Gaps 1;

Db 571 CAACGGCGCTTGCTGAGATCACCGAGATGATCCTGAGCATCCTCCACCGACGCAC 730
 529 CAGGACAGATGCCCTTTCGGAGATGGCATCGGCACTCGGCACTGGTCAGACGT 588
 Qy 731 GTTATCGACGCTTCGGAGACAGACAGAAACGCCAACATCGGAACACGGCATGGAAC 790
 Db 589 GTCATCGATCAGTGGACTTCGAGGCGCAAGGCCACGGCTGAATGCTCTGCAACCAC 648
 Qy 791 AAGTGGCGATTGGCTGTGATGTTCTGGACGGCGTGTGTCATGGAGG 850
 Db 649 AAGAGGTCAAAATGCTGTCGATACATCTATGATTCCTCGATATGATGCTGT 708
 Qy 851 TTGGCGAATCGGGGTTGGTGGATGTTGACCTTGTTGTTGTTGAAACTGGTAGGA 910
 Db 709 CTGGCCAGGATGATGAGATCTGTCAGATCTGACCGATTTGGTGGTCAGAAGTC 768
 Qy 911 GAGTCATGAGTCAAATACTCTTGTGATGATGCGATGGCTACGGCGACCGAGGA 970
 Db 769 GAGTCATGAGCTGGCTCAAGGGAAAGGA-----GAACGAG 807
 Qy 971 ACGTTGATFACTTTGAGAAGACTACTTGAGACTGAGCTGCTGTTGTCAGATG 1030
 Db 808 CGCTCTGCCATTACTGACCAAGCATACAGGAGACCATCGCTGATGCCATGCA 867
 Qy 1031 TGGAGAGCACTGGCTTCGGGTGTACGGCTGAGGTGGTGTGATCTGCTATGCT 1090
 Db 868 CTGGAGGCGACCGGGTGTGATGCCAGACGAGCAACCTGGGGGGCTTCAG 927
 Qy 1091 TACGGAGGAACTTGTGTTGGATTCAGATCTGAGACATCTGACTACCCGTC 1150
 Db 928 TACGGAGCAGACATCGCTGCTTCAGTGTGAGACATCTGACTTCAGTC 987
 Qy 1151 TCCCTTACCGACCTGGTAGGCCCGGGTGCAGCTCAAGCTGGTCTGGCCACCGG 1210
 Db 988 TCCACCGAGCAGATGGCAAGGCCGAGGGGGGATTTGAGCTGGTCTGGCCACCGT 1047
 Qy 1211 CCCGCCCTTCTGATGGAGAACACGCGCAGSTTGGTCCATGATAGCGAAGTC 1270
 Db 1048 CCCGRCCTCTTGTGAGAAGTACCCGAGCTGGTGTGATCCATGATGGGGCTC 1107
 Qy 1271 TCTGAGCCAGGAGGCTGGAGCTGGCTGACCGAGTTGGTGTGAGAAAGATGATGGATGGAG 1330
 Db 1108 AGCGGAGCCGGCAGCTGGAGACGCCCTTGAGCTGGTGACAGTCGACGGCTTGAG 1167
 Qy 1331 AAGGAGAGGCTGGGGAGAGATGCCAGAGGGCTGGTGTGAGATTCGAGGTC 1390
 Db 1168 CAGACCCGGTTCTGCCAAGAAGGACTGCAACGGGGCATACGGCTGCCAGGAGCTC 1227
 Qy 1391 CCGGAGAGTGGCGGAGGGCTGGAGCTGGTGTGACGGACAGAAGGTGTGA 1442
 Db 1228 CGGGAGTGGCTTACAGAAGGGTCTCCAGGTTGGCTGCCAGTGTACATCA 1279
 SQ

XX 06-MAR-2001 (first entry)
 DT
 XX DNA encoding straight-chain class prenyltransferase designated ATPt8.
 XX
 KW Prenyltransferase; ATPt1; ATPt2; ATPt3; ATPt4; ATPt5; ATPt6; ATPt7;
 KW ATPt8; ATPt9; ATPt10; ATPt11; ATPt12; tocopherol; homogentisic acid;
 KW phytolpyrophosphate; 2-methyl-6phytylbenzoquinol; antioxidant;
 KW nutritional supplement; ss.
 XX
 OS Arabidopsis sp.
 XX
 Key FH Location/Qualifiers
 CDS FT 1..956
 FT /itag= a
 FT /product= "prenyltransferase ATPt8"
 XX
 WO200063391-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US10363.
 XX
 PR 15-APR-1999; 99US-0129899.
 PR 30-JUL-1999; 99US-0146461.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 PI Savidge B, Lassner MW, Weiss JD, Post-Beittenmiller D;
 XX
 DR WPI; 2000-647519/62.
 DR P-PSDB; AAB19412.
 XX
 PT An isolated nucleic acid sequence encoding prenyltransferase used to transform plant cells to increase the production of tocopherols -
 XX
 PS Example 1; Page 82; 114pp; English.
 XX
 The present sequence encodes a prenyltransferase. The specification describes prenyltransferases designated ATPt1, ATPt2, ATPt3, ATPt4, ATPt5, ATPt6, ATPt7, ATPt8, ATPt9, ATPt10, ATPt11, and ATPt12. The biosynthesis of alpha-tocopherol in higher plants involves the condensation of homogentisic acid and phytolpyrophosphate to form 2-methyl-6phytylbenzoquinol, which can form various tocopherols. The prenyltransferase polynucleotides are useful in transforming host cells to alter the expression of prenyltransferase in these cells. The transformed cells are used in the production of tocopherols which are of use in the pharmaceutical industry as antioxidants and also in the food industry as nutritional supplements.

XX Sequence 966 BP; 278 A; 196 C; 240 G; 252 T; 0 other;
 SQ
 Query Match 10.9%; Score 180.8; DB 21; Length 966;
 Best Local Similarity 54.1%; Pred. No. 1.e-36; Matches 405; Conservative 0; Mismatches 322; Indels 21; Gaps 1;

Qy 650 ACGTGAATATCCCTGCCCTCGACGGGGTGGCTGAGATACGGAGATGTCATGCA 709
 Db 163 ACATCAGATTAGCGCTGGAGGAACGGGTATGCTGAAATCTGAAATGATGATACGTC 222
 Qy 710 GCATCACTCTCCACGAGCACCTATGACGCTTCCGGAGACAGAACACCATCC 769
 Db 223 CGAAGTCACTGACGATGATGCTTGGATGTCGCAATACGGCTGCCAGGAGCTC 282
 Qy 770 GAAACAGGAGCTCGAAACAGATGGCATTTGGCTGGGATTTCTGGGACCG 829
 Db 283 TAATGTTGTAATGGTACAAGATGTTGTTAGCAGGAGCTTCTGCTCCCG 342
 Qy 830 GCGCTGTTGCTGGAGGTGCGAATCCGGAGGTGATGAGCTTGTGACTCTGTT 889
 Db 343 GCTTGCGGCTCTGCGCTTAAAGACACAGAGCTGTTGCAACTGCT 402
 Qy 890 ATGCAAATCTGGTGAAGGAGAGTCACTGCACTGTGAAATAACTGTTGATGATGCCATT 949
 RESULT 15
 AAC61900 AAC61900 standard; DNA; 966 BP.
 ID AAC61900
 XX AAC61900;

Db 403 GAGAACATCTTACGGTAAACCATGAAATACTG----- 444
 Qy 950 GAGGTAGGCAGCGAGAAAGTTGAGACTTACTTGAAAGACT 1009
 Db 445 -- TCAACCGAGCAGCGTTATGATGACTACATGAGA----- 501
 Qy 1010 GCCTCCCTGATTCCCAAAGTCGTCAGCCAAGTGCGCTTCTGGTGGTAGCCTGAG 1069
 Db 502 GATCGTAATCTTACGTCGAANGCTGCAACTGACAGAGAA 561
 Qy 1070 GTTGCTGATGCTGCTTATGCTTACGGAAAGAACCTTGTTGGCATCCAGATCGTCGAC 1129
 Db 562 GTTGCCGTTGCTTGAATGGGAAATCTGGTTTGCATTCAAATAAGAC 621
 Qy 1130 GAGATGCTGACTACCGTCTCGTACCGTCTGGTAACCCGGTCAAGCTTCACGCTC 1189
 Db 622 GACATTCTGATTTCAGGGCACATCTGCCCTCTCGAAAGGGATCTGGTCAAGTATT 681
 Qy 1190 CAGCTCGCTCGGCCACCGGCCCTCTGATGAAACCAAGCCCAGCTGGT 1249
 Db 682 CGCCATGGTATAAAGCCCCAATCTCTGAGGTTCCCTAACAGC 741
 Qy 1250 CCCATGATCAAGCCAAAGTCTCTGACCCAGGAGCTGCCAGCTGCAAGCTGGTC 1309
 Db 742 GAGTTGGTGAATGAAAGATCTCTGAAATCTTGACATTGGATATCTT 801
 Qy 1310 GCGAAAGTGAAGTGGATGGAGAGACGAGGCTTGCCAGANGCG 1369
 Db 802 GCGAAGAGCAAGGAAATACGGGGCAAGGAAATTAGCCATGGAACATGGGAATCTAGCA 861
 Qy 1370 TGGATGCAATTGGACGTTCCGGAGA 1397
 Db 862 CGAGCTGAAATGGGTCTACTGAA 889

Search completed: January 16, 2003, 08:23:14
 Job time : 277 secs

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Result No.	Score	Query	Match	Length	DB ID	Description
C 1	179.2	10.8	5926	4	US-09-027-169-3	Sequence 3, Appli
C 2	179.2	10.8	5926	4	US-09-027-169-4	Sequence 4, Appli
C 3	160.4	9.7	3301	2	US-08-447-430A-42	Sequence 2, Appli
C 4	155.2	9.4	4009	2	US-08-500-860A-2	Sequence 40, Appli
C 5	152.4	9.2	3423	2	US-08-447-430A-40	Sequence 86, Appli
C 6	152.4	9.2	3423	4	US-08-485-737B-86	Sequence 7, Appli
C 7	152	9.2	1097	2	US-08-761-258-7	Sequence 7, Appli
C 8	152	9.2	1097	2	US-08-977-306-7	Sequence 3, Appli
C 9	148.8	9.0	6312	1	US-08-531-601-3	Sequence 10, Appli
C 10	148.8	9.0	6312	2	US-08-859-032-3	Sequence 3, Appli
C 11	147.2	8.9	518	4	US-09-242-901-3	Sequence 3, Appli
C 12	147	8.9	3423	4	US-08-447-430A-41	Sequence 4, Appli
C 13	147	8.9	3474	2	US-08-318-837-10	Sequence 10, Appli
C 14	147	8.9	3474	4	US-08-122-458D-8	Sequence 8, Appli
C 15	147	8.9	8430	4	US-08-131-028A-6	Sequence 6, Appli
C 16	147	8.9	8430	4	US-09-131-028A-10	Sequence 10, Appli
C 17	146.2	8.8	628	4	US-09-242-901-1	Sequence 1, Appli
C 18	146	8.8	4476	3	US-08-801-344-2	Sequence 2, Appli
C 19	146	8.8	4476	4	US-09-498-599-2	Sequence 2, Appli
C 20	145.6	8.8	7475	2	US-08-971-036-1	Sequence 1, Appli
C 21	145.6	8.8	7475	3	US-08-096-570-1	Sequence 1, Appli
C 22	145.6	8.8	7475	4	US-09-265-617B-1	Sequence 2, Appli
C 23	145.4	8.8	1200	4	US-09-204-117B-2	Sequence 3, Appli
C 24	145.4	8.8	2650	4	US-09-204-117B-3	Sequence 3, Appli
C 25	145.4	8.8	4199	4	US-09-204-117B-1	Sequence 1, Appli
C 26	144	8.7	5096	1	US-08-105-433A-3	Sequence 3, Appli
C 27	144	8.7	5110	1	US-08-105-433A-4	Sequence 4, Appli

GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

Run on: January 16, 2003, 07:27:51 ; Search time 58 Seconds
(without alignments)
8740.288 Million cell updates/sec

Title: US-09-830-111A-1
Perfect score: 1653
Sequence: 1 ttttgtggggcgaaaatcaggaaatggatgaa 1653

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-09-027-169-3/c
; Sequence 3, Application US-09027169
; Patent No. 6420524
; GENERAL INFORMATION:
; APPLICANT: CRAIG, NANCY L.
; TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Brown (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave.
; CITY: Raleigh
; STATE: NC
; COUNTRY: USA
; ZIP: 27608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-09-027-169
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-3

RESULT 2
US-09-027-169-4
; Sequence 4, Application US-09-027-169-4
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 4:
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; TOPOLOGY: circular
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; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-4

RESULT 3
US-09-027-169-4
; Sequence 2, Application US-09-027-169-4
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
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; SEQUENCE CHARACTERISTICS:
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; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-2

RESULT 4
US-09-027-169-2
; Sequence 1, Application US-09-027-169-2
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

RESULT 5
US-09-027-169-1
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
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; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

RESULT 6
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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; TELEPHONE: 919 420 2205
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; US-09-027-169-1

RESULT 7
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; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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; US-09-027-169-1

RESULT 8
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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; TELEPHONE: 919 420 2205
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; US-09-027-169-1

RESULT 9
US-09-027-169-1
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
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; REFERENCE DOCKET NUMBER: 5789-3
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; US-09-027-169-1

RESULT 10
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; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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; US-09-027-169-1

RESULT 11
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; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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; US-09-027-169-1

RESULT 12
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
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; US-09-027-169-1

RESULT 13
US-09-027-169-1
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
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; US-09-027-169-1

RESULT 14
US-09-027-169-1
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
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; US-09-027-169-1

RESULT 15
US-09-027-169-1
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; FILING DATE:
; CLASSIFICATION: 435
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; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
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RESULT 16
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; FILING DATE:
; CLASSIFICATION: 435
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; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
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; US-09-027-169-1

RESULT 17
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; REGISTRATION NUMBER: 36,463
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RESULT 18
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; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
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RESULT 19
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
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RESULT 20
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
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RESULT 21
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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RESULT 22
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
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RESULT 23
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
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RESULT 24
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

RESULT 25
US-09-027-169-1
; Sequence 1, Application US-09-027-169-1
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

RESULT 26
US-09-027-169-1
; Sequence 1, Application US-09-027-169-1
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

RESULT 27
US-09-027-169-1
; Sequence 1, Application US-09-027-169-1
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
; US-09-027-169-1

QY 1506 GCAAGCTGGCTTTCGGCATGAGAGATTTCAGSCTGTACAGATAATCAG 1565
Db 4222 GCAAGCTGGCTTTCGGCATGAGAGATTTCAGSCTGTACAGATAATCAG 4163

RESULT 3
US-08-447-430A-42
; Sequence 42, Application US/08447430A

QY 1566 AACGAGAAGGGTCTGATAMACAGAATTGCCCTGGCGAGTGGCGGTGGCCAC 1625
Db 4162 AACGAGAAGGGTCTGATAMACAGAATTGCCCTGGCGAGTGGCGGTGGCCAC 4103

QY 1626 CTGACCCATGCGGAACTCAGAGTGAA 1653
Db 4102 CTGACCCATGCGGAACTCAGAGTGAA 4075

RESULT 2
US-09-027-169-4/c
; Sequence 4, Application US/09027169

Patent No. 6420524

GENERAL INFORMATION:
APPLICANT: CRAIG, NANCY L
TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Brown (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave.
CITY: Raleigh
STATE: NC
COUNTRY: USA
ZIP: 27608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,169
FILING DATE: 2001-01-10
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE DOCKET NUMBER: 5789-3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2205
TELEFAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 3301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular

MOLECULE TYPE: plasmid vector
HYPOTHETICAL: No

US-08-447-430A-42

Query Match 9 7%; Score 160.4; DB 2; Length 3301;
Best Local Similarity 97.8%; Pred. No. 9e-33; 1; Indels 3; Gaps 1;
Matches 174; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1476 GGGGATCTCTAGTGGCTGACCTSCAGGCATGCGAGCTGGCTTGGCGATGAGGA 1535
Db 237 GGGGATCTCTAGTGGCTGACCTSCAGGCATGAGGA 293

QY 1536 AGATTTCACTCTATCGATTAATCGAGGAGAGGGCTGATAAACAGATT 1595
Db 294 AGATTTCACTCTATCGATTAATCGAGGAGAGGGCTGATAAACAGATT 353

QY 1596 TGCCCTGGCGAGTAGCGCGGTGGTCCCACCTGACCTCGCGGAACTCAGAGTGAA 1653
Db 354 TGCCCTGGCGAGTAGCGCGGTGGTCCCACCTGACCTCGCGGAACTCAGAGTGAA 411

RESULT 4
US-08-500-860A-2
; Sequence 2, Application US/08500860A

Patent No. 5891679

GENERAL INFORMATION:
APPLICANT: LUCAS, RUDOLPH
APPLICANT: DE BAESBELIE, PATRICK
APPLICANT: FRANSSEN, LUCIE
APPLICANT: SABRON, ERWIN

APPLICANT: THERMOPHILIC BACTERIA FOR PREPARING TNF-MUTINS, A PROCESS FOR PREPARING THEM AND THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: TNF-MUTINS, A PROCESS FOR PREPARING THEM AND THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.

STREET: 1100 NORTH GLENBEE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

QY 1626 CTGACCCATGCGGAACTCAGAGTGAA 1653
Db 3738 CTGACCCATGCGGAACTCAGAGTGAA 3711

QY 1566 AACGAGAAGGGTCTGATAMACAGAATTGCCCTGGCGAGTGGCGGTGGCCAC 1625
Db 3918 GTTATTAAGGTCTGACGACTTCTGGGATCTAGATGACCTCGAGGCACT 3859

QY 1506 GCAAGCTGGCTTTCGGCATGAGAGATTTCAGSCTGTACAGATAATCAG 1565
Db 3858 GCAAGCTGGCTTTCGGCATGAGAGATTTCAGSCTGTACAGATAATCAG 3799

QY 1566 AACGAGAAGGGTCTGATAMACAGAATTGCCCTGGCGAGTGGCGGTGGCCAC 1625
Db 3798 AACGAGAAGGGTCTGATAMACAGAATTGCCCTGGCGAGTGGCGGTGGCCAC 3739

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/500,860A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: TYRN, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)816-4000
 TELEX: (703)816-4100
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 4009 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: PIG2
 US-08-500-860A-2

Query Match 9.4%; Score 155.2; DB 2; Length 4009;
 Best Local Similarity 96.6%; Pred. No. 2.3e-31; Indels 3; Gaps 1;
 Matches 170; Conservative 0; Mismatches 3;

Qy 1478 GGATCCCTAGTCGACTCGAGCATGGTGTGGCTGGATGAGGAAG 1537
 Db 947 GAATTCTCTAGTCGACTCGAGCC---CRAACTTGCTGTGTTGGGGATGAGGAAG 1003

Qy 1538 ATTTTCAGCCCTAGACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTG 1597
 Db 1004 ATTTTCAGCCCTAGACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTG 1063

Qy 1598 CCTGGCGGCAGTAGGCCGGTGTGGTCCCACCTGACCCATGCCAACCTAGAAACTGAA 1653
 Db 1064 CCTGGCGGCAGTAGGCCGGTGTGGTCCCACCTGACCCATGCCAACCTAGAAACTGAA 1119

RESULT 5
 US-08-447-430A-40
 Sequence 40, Application US/08447430A
 Patent No. 591658
 GENERAL INFORMATION:
 APPLICANT: Recombinant polypeptides and peptides,
 TITLE OF INVENTION: recombinant nucleic acids coding for the same and use of these
 TITLE OF INVENTION: peptides and peptides in the diagnostic of
 TITLE OF INVENTION: tuberculosis.
 NUMBER OF SEQUENCES: 43
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/447,430A
 FILING DATE:
 CLASSIFICATION: 424
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3423 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: plasmid vector
 HYPOTHETICAL: NO
 US-08-447-430A-40

Query Match 9.2%; Score 152.4; DB 2; Length 3423;
 Best Local Similarity 97.6%; Pred. No. 1.2e-30; Indels 3; Gaps 1;
 Matches 166; Conservative 0; Mismatches 1;

Qy 1484 TCTAGAGTCGACCTGCAAGCATGGCTGGCTGGGATGAGGAAGATTTC 1543
 Db 363 TCTAGAGTCGACCTGAGCC---CRAACTTGCTGTGTTGGGGATGAGGAAGATTTC 419

Qy 1544 AGCCTGATACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTGCTGGC 1603
 Db 420 AGCCTGATACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTGCTGGC 479

Qy 1604 GGCAGTAGCGCGTGTGGTCCCACCTGACCCATGCCAACCTGACCCATGCCAACCTGACAACTGAA 1653
 Db 480 GGCAGTAGCGCGTGTGGTCCCACCTGACCCATGCCAACCTGACCCATGCCAACCTGACAACTGAA 529

RESULT 6
 US-09-485-737B-86
 Sequence 86, Application US/09485737B
 Patent No. 6350860
 GENERAL INFORMATION:
 APPLICANT: Buyse, Marie-Ange
 APPLICANT: Sblon, Ervin
 TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
 FILE REFERENCE: INNS:015
 CURRENT APPLICATION NUMBER: PCT/EP 98/05165
 PRIOR APPLICATION NUMBER: PCT/EP 98/05165
 PRIOR FILING DATE: 1998-08-14
 PRIOR APPLICATION NUMBER: EPO 98870139-7
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: EPO 97870122-5
 PRIOR FILING DATE: 1997-08-18
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 86
 LENGTH: 3423
 TYPE: DNA
 ORGANISM: UNKNOWN
 FEATURE:
 OTHER INFORMATION: GENOMIC
 US-09-485-737B-86

Query Match 9.2%; Score 152.4; DB 4; Length 3423;
 Best Local Similarity 97.6%; Pred. No. 1.2e-30; Indels 3; Gaps 1;
 Matches 166; Conservative 0; Mismatches 1;

Qy 1484 TCTAGAGTCGACCTGCAAGCATGGCTGGCTGGGATGAGGAAGATTTC 1543
 Db 363 TCTAGAGTCGACCTGAGCC---CRAACTTGCTGTGTTGGGGATGAGGAAGATTTC 419

Qy 1544 AGCCTGATACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTGCTGGC 1603
 Db 420 AGCCTGATACATTAATCAGAACCGAGGGTCTGATAAAACAGAATTGCTGGC 479

Qy 1604 GGCAGTAGCGCGTGTGGTCCCACCTGACCCATGCCAACCTGACCCATGCCAACCTGACAACTGAA 1653
 Db 480 GGCAGTAGCGCGTGTGGTCCCACCTGACCCATGCCAACCTGACCCATGCCAACCTGACAACTGAA 529

RESULT 7
 US-08-761-258-7
 Sequence 7, Application US/08761258
 Patent No. 5756087
 GENERAL INFORMATION:
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Torkewitz, Nancy
 TITLE OF INVENTION: Genetically Modified Pseudomonas Strains

TITLE OF INVENTION: with Enhanced Biocontrol Activity
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Ciba-Geigy Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,258
 FILING DATE:

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Meij, J. Timothy
 REGISTRATION NUMBER: 38,241
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-5897
 TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1097 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 IMMEDIATE SOURCE:
 CLONE: DKK223-3

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1086

OTHER INFORMATION: /note= "BglI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1092

OTHER INFORMATION: /note= "HindIII site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1086

OTHER INFORMATION: /note= "BglI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1092

OTHER INFORMATION: /note= "HindIII site"

FEATURE:
 NAME/KEY: promoter
 LOCATION: 185..264

OTHER INFORMATION: /standard_name= "tac"

FEATURE:
 NAME/KEY: terminator
 LOCATION: 327..752

OTHER INFORMATION: /standard_name= "rrnB"

US-08-761-258-7

Query Match 9.2%; Score 152; DB 1; Length 1097;
 Best Local Similarity 77.1%; Pred. No. 1e-30; Matches 185; Conservative 0; Mismatches 55; Indels 0; Gaps 0; Matches 185; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1414 TTGGAGCAGTGTACGGCAAGGTTGACTCGTCAGATGGAAATTGACACTCGGATAC 1473
 Db 225 TGTGGATCTGACGGATTAACATTACACAGGAACAGAATTCCGGGATCCGTG 284

QY 1474 CCGGGATCTCTAGAGTCGACCTGCAGCGATCAACATTGCGTGTGTGGGGATGAGA 1533
 Db 285 ACCTGCAGTCAGACTCGAGGGTACCGGGCGCGCAAGCTTGCTGTG 344

QY 1534 GAAGATTTGCGCTGATCAGATAAACATCGAACGCGAAGGGTCTGATTAACAGAA 1593
 Db 345 GAAGATTTGCGCTGATCAGATAAACATCGAACGCGAAGGGTCTGATTAACAGAA 404

QY 1594 TTGGCTGGCGCGAGTAGGGGGTGTCCACCTGACCCCATGCCGACTCGAGTGA 1653
 Db 405 TTGGCTGGCGAGTAGGGGGTGTCCACCTGACCCCATGCCGACTCGAGTGA 464

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 270
 OTHER INFORMATION: /note= "SmaI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 275
 OTHER INFORMATION: /note= "BamHI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 281
 OTHER INFORMATION: /note= "SalI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 287
 OTHER INFORMATION: /note= "PstI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 293
 OTHER INFORMATION: /note= "XbaI site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 299
 OTHER INFORMATION: /note= "Khol site"

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 305
 OTHER INFORMATION: /note= "KpnI site"

RESULT 8
 US-08-977-3-06-7

Sequence 7, Application US/08977306
 Patent No. 5955348

GENERAL INFORMATION:

APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Torkewitz, Nancy
 APPLICANT: Stafford, Jill M.

TITLE OF INVENTION: Genetically Modified Pseudomonas Strains with Enhanced Biocontrol Activity

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ADDRESSE: No. 5955348artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/977,306
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38 241
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
IMMEDIATE SOURCE:
CLONE: pRK223-3
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "BssHII site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7
OTHER INFORMATION: /note= "BgIII site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 265
OTHER INFORMATION: /note= "ECORI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 270
OTHER INFORMATION: /note= "BssHII site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 275
OTHER INFORMATION: /note= "BamHI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 281
OTHER INFORMATION: /note= "SalI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 287
OTHER INFORMATION: /note= "PstI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 293
OTHER INFORMATION: /note= "XbaI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 299
OTHER INFORMATION: /note= "KpnI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 311
OTHER INFORMATION: /note= "XhoI site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 319
OTHER INFORMATION: /note= "No. 5955348I site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 327
OTHER INFORMATION: /note= "BglII site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1086
OTHER INFORMATION: /note= "BgIII site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1092
OTHER INFORMATION: /note= "BssHII site"

OTHER INFORMATION: /note= "BssHII site"
FEATURE:
NAME/KEY: promoter
LOCATION: 185..264
OTHER INFORMATION: /standard_name= "lac"
FEATURE:
NAME/KEY: terminator
LOCATION: 327..752
OTHER INFORMATION: /standard_name= "rrnB"
US-08-977-306-7

OTHER INFORMATION: /note= "BssHII site"
FEATURE:
NAME/KEY: promoter
LOCATION: 185..264
OTHER INFORMATION: /standard_name= "lac"
FEATURE:
NAME/KEY: terminator
LOCATION: 327..752
OTHER INFORMATION: /standard_name= "rrnB"
US-08-977-306-7

Query Match 9.2%; Score 152; DB 2; Length 1097;
Best Local Similarity 77.1%; Pred. No. 1e-30;
Matches 185; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 1414 TTGGGACAGTGTGACCGAACAGGTGTTGACTAGGTAAGATAAGCTGGCTGGTCGGTAC 1473
Db 225 TGTGGATGTGAGCGATTAACAAATTCAACAGGAAACAGAATTCGGGATTCGGTCG 284

Qy 1474 CGGGGATCCCTAGACTGACCTGGCATGCAACCTGGCTGGCTGGGGATGAGA 1533
Db 285 ACCTGAGCTGTAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 344

Qy 1534 GAAGATTTCAGCCTGATACAGATTAATCAGAACCGAACGGCTCTGATAAAACAGAA 1593
Db 345 GAAGATTTCACCCGTGATACAGATTAATCAGAACCGAACGGCTCTGATAAAACAGAA 404

Qy 1594 TTGGCTTGCGCGCAGTAGCGCGTGGTCCCACCTGACCCATGCCAACTAGAAAGTGA 1653
Db 405 TTGCTTGCGGCCAGTAPCGCGGTGGTCCACCTGACCCATGCCAACTAGAAAGTGA 464

RESULT 9
US-08-331-601-3
Sequence 3, Application US/08531601
Patent No. 568864
GENERAL INFORMATION:
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: MAEBA, HIROO
APPLICANT: OKADA, YUKIO
TITLE OF INVENTION: RECOMBINANT BETA-AMYLASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPOVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,601
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI 6-233086
FILING DATE: 28-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 081531,601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: 248555 OPAT UR
TELEX: 248555 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6312 base pairs
TYPE: nucleic acid

```

;

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-531-601-3

Query Match 9.0%; Score 148.8; DB 1; Length 6312;

Best Local Similarity 98.7%; Pred. No. 1.3e-29;

Matches 150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

;

Qy 1502 GCATCGCAAGCTTGCTGTTGGGATGAGAGAAGATTTCAGCCGTATAACAGATTA 1561

Db 1747 GCAGCCAAGCTTGCTGTTGGGATGAGAGAAGATTTCAGCCGTATAACAGATTA 1806

Qy 1562 TAGAACGGAGAGGGCTGATAAACAGCATGAGATTCAGCTGATAACAGATTA 1621

Db 1807 TCAGAACCCAGAGGGCTGATAAACAGATTCAGCTGCGGGAGTAGCGCGTGGTC 1866

Qy 1622 CACACTGACCCATGCCGAACTCAGAAGTGA 1653

Db 1867 CCACCTGACCCATGCCGAACTCAGAAGTGA 1898

;

RESULT 10

US-08-859-032-3

Sequence 3, Application US/08859032

Patent No. 5863784

GENERAL INFORMATION:

APPLICANT: YOSHIGI, NACHIRO

APPLICANT: MAREBA, HIDEO

APPLICANT: OKADA, YUKIO

APPLICANT: OBLON, SPIVAK, MCCLELLAND, MAYER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VIRGINIA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,032

APPLICATION NUMBER: US/08/859,032

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/531,601

FILED DATE: 21-SEP-1995

APPLICATION NUMBER: JP HEI 6-233086

FILED DATE: 28-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 08/531,601

REFERENCE/DOCKET NUMBER: 2589-031-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 6312 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-859-032-3

Query Match 9.0%; Score 148.8; DB 2; Length 6312;

Best Local Similarity 98.7%; Pred. No. 1.3e-29;

Matches 150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

;

RESULT 11

US-09-242-901-3

Sequence 3, Application US/09242901

Patent No. 6322783

GENERAL INFORMATION:

APPLICANT: TAKAHASHI, SEISHI

TITLE OF INVENTION: NOVEL BACTERIOPHAGES, METHOD FOR SCREENING SAME AND DETECTION

TITLE OF INVENTION: KITS USING SAME

FILE REFERENCE: 300-001

CURRENT APPLICATION NUMBER: US/09/242,901

CURRENT FILING DATE: 1999-02-26

EARLIER APPLICATION NUMBER: PCT/JP97/02957

EARLIER FILING DATE: 1997-08-26

EARLIER APPLICATION NUMBER: 8/261132

EARLIER FILING DATE: 1995-08-26

EARLIER FILING DATE: 1997-04-19

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 518

TYPE: DNA

ORGANISM: Bacteriophage

FEATURE:

OTHER INFORMATION: "n" at various positions throughout the sequence may be

US-09-242-901-3

Query Match 8.9%; Score 147.2; DB 4; Length 518;

Best Local Similarity 98.0%; Pred. No. 1.4e-29;

Matches 149; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

;

Qy 1502 GCATCGCAAGCTTGCTGTTGGGATGAGAGAAGATTTCAGCCGTATAACAGATTA 1561

Db 189 GAAAGAAGAGCTTGCTGTTGGGATGAGAGAAGATTTCAGCCGTATAACAGATTA 248

Qy 1562 TCAGAACCGAGAACGGCTGATAAACAGAATTGCCTGGGGAGTAGCCGGTGGTC 1621

Db 249 TCAGAACCGAGAACGGCTGATAAACAGAATTGCCTGGGGAGTAGCCGGTGGTC 308

Qy 1622 CACACTGACCCATGCCGAACTCAGAAGTGA 1653

Db 309 CCACCTGACCCATGCCGAACTCAGAAGTGA 340

;

RESULT 12

US-08-447-430A-41

Sequence 41, Application US/08447430A

Patent No. 5916558

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Recombinant polypeptides and peptides, nucleic acids coding for the same and use of these

TITLE OF INVENTION: polypeptides and peptides in the diagnostic of tuberculosis.

TITLE OF INVENTION: tuberculosis.

NUMBER OF SEQUENCES: 43

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,430A
FILING DATE:

CLASSIFICATION: 424
SEQUENCE CHARACTERISTICS:
LENGTH: 3474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: plasmid vector
HYPOTHETICAL: NO

US-08-447-430A-41

Query Match Score 8.9%; Score 147; DB 2; Length 3474;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1507 CAAGCTTGCCTTTCGGATGAGAAATTTCAGCTGTATACTGATAATCAGA 1566
Db 436 CAAGCTTGCCTTTCGGATGAGAAATTTCAGCTGTATACTGATAATCAGA 495

Qy 1567 AGCGAGAAGGCTCTGATAAACAGAAATTTCGCTGGGGCACTAGGCCGGTGGTCCACC 1626
Db 496 AGCGAGAAGGCTCTGATAAACAGAAATTTCGCTGGGGCACTAGGCCGGTGGTCCACC 555

Qy 1627 TGACCCCCATGCCGAACCTAGAGTCAA 1653
Db 556 TGACCCCCATGCCGAACCTAGAGTCAA 582

RESULT 14
US-08-122-458D-8

Sequence 8, Application US/08122458D
Patent No. 6387372

GENERAL INFORMATION:
APPLICANT: Cocito, Carlo
APPLICANT: Coene, Marc
APPLICANT: DeKesel, Myriam
APPLICANT: Gilot, Philippe
TITLE OF INVENTION: Polypeptides from Mycobacterium
TITLE OF INVENTION: Paratuberculosis
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6387372west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,458D
FILING DATE: 24-SEP-1993
CLASSIFICATION: 425
PRIORITY DATA:
APPLICATION NUMBER: EP 91400798.4
FILING DATE: 25-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.111USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-3081
INFORMATION FOR SEQ ID NO: 8:

TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: pmTNF-MPH
; US-08-318-837-10

Query Match Score 8.9%; Score 147; DB 2; Length 3474;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1507 CAAGCTTGCCTTTCGGATGAGAAATTTCAGCTGTATACTGATAATCAGA 1566
Db 436 CAAGCTTGCCTTTCGGATGAGAAATTTCAGCTGTATACTGATAATCAGA 495

Qy 1567 AGCGAGAAGGCTCTGATAAACAGAAATTTCGCTGGGGCACTAGGCCGGTGGTCCACC 1626
Db 496 AGCGAGAAGGCTCTGATAAACAGAAATTTCGCTGGGGCACTAGGCCGGTGGTCCACC 555

Qy 1627 TGACCCCCATGCCGAACCTAGAGTCAA 1653
Db 556 TGACCCCCATGCCGAACCTAGAGTCAA 582

RESULT 14
US-08-122-458D-8

Sequence 8, Application US/08122458D
Patent No. 6387372

GENERAL INFORMATION:
APPLICANT: Cocito, Carlo
APPLICANT: Coene, Marc
APPLICANT: DeKesel, Myriam
APPLICANT: Gilot, Philippe
TITLE OF INVENTION: Polypeptides from Mycobacterium
TITLE OF INVENTION: Paratuberculosis
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6387372west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,458D
FILING DATE: 24-SEP-1993
CLASSIFICATION: 425
PRIORITY DATA:
APPLICATION NUMBER: WO PCT/EP92/00661
FILING DATE: 24-MAR-1992
PRIORITY DATA:
APPLICATION NUMBER: EP 91400798.4
FILING DATE: 25-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.111USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-3081
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3474 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-122-458D-8

Query Match 8.9%; Score 147; DB 4; Length 3474;
 Best Local Similarity 100.0%; Pred. No. 3.1e-29; Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Type: nucleic acid
 Strandedness: double
 Topology: linear
 Molecule Type: DNA (genomic)
 US-08-122-458D-8

RESULT 15
 US-09-131-028A-6/C
 Sequence 6, Application US/09131028A
 Patent No. 6287865
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Lemmel, Steven A.
 APPLICANT: Leonard, Amanda Eun-Yeong
 APPLICANT: Chaudhary, Sunita
 TITLE OF INVENTION: BETA-CASEIN EXPRESSING CONSTRUCTS
 FILE REFERENCE: 6004.US.PI
 CURRENT APPLICATION NUMBER: US 09/131,028A
 CURRENT FILING DATE: 1998-08-07
 PRIOR APPLICATION NUMBER: US 08/064,440
 PRIOR FILING DATE: 1993-05-21
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 8430
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (6124)..(6939)
 OTHER INFORMATION: KANR - kanamycin resistance in forward orientation
 US-09-131-028A-6

Query Match 8.9%; Score 147; DB 4; Length 8430;
 Best Local Similarity 100.0%; Pred. No. 4.1e-29; Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Type: nucleic acid
 Strandedness: double
 Topology: linear
 Molecule Type: DNA (genomic)
 US-09-131-028A-6

Query Match 8.9%; Score 147; DB 4; Length 8430;
 Best Local Similarity 100.0%; Pred. No. 4.1e-29; Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Type: nucleic acid
 Strandedness: double
 Topology: linear
 Molecule Type: DNA (genomic)
 US-09-131-028A-6

QY 1507 CAAGCTTGGCTTGGGATGAGAAAGATTTCAGCTGATAACAGTTAACATCAGA 1566
 Db 436 CAAGCTTGGCTTGGGATGAGAAAGATTTCAGCTGATAACAGTTAACATCAGA 495

QY 1567 ACGGAGAACGGCTGTGATAAACAGATTGCCTGGGGCACTAGAGCGGTGGCCACC 1626
 Db 496 ACGGAGAACGGCTGTGATAAACAGATTGCCTGGGGCACTAGAGCGGTGGCCACC 555

QY 1627 TGACCCCATGCCGAACCTAGAGTCAA 1653
 Db 556 TGACCCCATGCCGAACCTAGAGTCAA 582

Search completed: January 16, 2003, 08:53:08
 Job time : 88 secs

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OM nucleic - nucleic search, using bw model

Run on: January 16, 2003, 08:18:51 ; Search time 70 Seconds
(without alignments)

10528.861 Million cell updates/sec

Title: US-09-830-111A-1

Perfect score: 1653

Sequence: 1 tttttgtgggtcgaaaaagtcc.....atggccaaactcaggagtcaa 1653

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 393868 seqs, 22934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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10: /cgn2_6_ptodata/2/pubpna/US09_PUBCOMB.seq*
11: /cgn2_6_ptodata/2/pubpna/US10_NEW_PUB.seq*
12: /cgn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq*
13: /cgn2_6_ptodata/2/pubpna/US60_NEW_PUB.seq*
14: /cgn2_6_ptodata/2/pubpna/US60_PUBCOMB.seq*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	179.2	10.8	5926	9 US-10-024-809-3	Sequence 3, Appli
C 2	179.2	10.8	5926	9 US-10-024-809-4	Sequence 4, Appli
C 3	145.4	8.8	6271	10 US-09-993-292A-1	Sequence 1, Appli
C 4	145.4	8.8	8908	10 US-19-993-292A-18	Sequence 10, Appli
C 5	138	8.3	425	10 US-09-960-428-10	Sequence 10, Appli
6	136	8.2	1173	10 US-09-887-576-678	Sequence 678, App
7	136	8.2	1179	9 US-09-938-842A-990	Sequence 990, App
8	130.8	7.9	7416	10 US-09-900-575-46	Sequence 46, Appli
9	120.8	7.3	894	9 US-09-938-842A-1124	Sequence 1124, Appli
10	115.4	7.0	799	10 US-09-912-020-27	Sequence 27, Appli
11	79.2	4.8	927	10 US-09-974-300-999	Sequence 999, App
12	68.2	4.1	972	10 US-09-815-242-9636	Sequence 9636, App
13	64.2	3.9	767	12 US-10-04-037-1	Sequence 1, Appli
14	63	3.8	1323	12 US-10-03-036-3	Sequence 3, Appli
C 15	61.6	3.7	103	10 US-09-179-5136B-267	Sequence 267, App
C 16	61.6	3.7	513	10 US-09-974-300-5444	Sequence 5444, App
C 17	61.6	3.7	1361	10 US-09-393-634-14	Sequence 14, Appli
C 18	61.4	3.7	293	9 US-10-132-561-11	Sequence 11, Appli
C 19	61.4	3.7	293	9 US-10-132-561-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-10-024-809-3/c

; Sequence 3, Application US/10024809
; Publication No. US20020188105A1
; GENERAL INFORMATION:
; APPLICANT: CRAIG, NANCY L.
; TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
; ATP-DEPENDENT TRANPOSITION PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Brown (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave.
; CITY: Raleigh
; STATE: NC
; COUNTRY: USA
; ZIP: 27608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10-024-809
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/027,169
; FILING DATE: 1998-FEB-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 5789-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2205
; TELEFAX: 919 81 3175
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: /desc = "DEM delta R.adj to 1"
; US-10-024-809-3

DESCRIPTION: SEQ ID NO: 3:

Query Match 10.8%; Score 179.2; DB 9; length 5926;
Best Local Similarity 91.3%; Pred. No. 6.5e-45;
Matches 190; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1446 GGTCAAGATGGAATTGAGCTGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCA 1505
Db 4282 GTTTAATTAAGCTGTGCGAACGGACTTCTGGGATCTCTAGAGTCGACCTGCAGGCA 4223

QY 1506 GCAAGCTGGCTTTCGGGATGAGAGAGATTTCAGCTGATACAGATAATCAG 1565
Db 4222 GCAAGCTGGCTTTCGGGATGAGAGAGATTTCAGCTGATACAGATAATCAG 4103

QY 1566 AACGGAGAGGGCTCGATAAACAGAAATTGCGCTGGGGAGTAGGGGGGTCCAC 1625
Db 3798 AACGGAGAGGGCTCGATAAACAGAAATTGCGCTGGGGAGTAGGGGGGTCCAC 3739

QY 1626 CTGACCCCAGGCCGAACTCAGAGTGA 1653
Db 4102 CTGACCCCAGGCCGAACTCAGAGTGA 4075

RESULT 2
US-10-024-809-4/C
; Sequence 4, Application US/10024809
; Publication No. US200201488105A1

GENERAL INFORMATION:
; APPLICANT: CRAIG, NANCY L
; TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Brown (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave.
; CITY: Raleigh
; STATE: NC
; ZIP: 27608

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM C compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/024, 809
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/027, 169
; FILING DATE: 199-FEB-20

ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36, 463
; REFERENCE/DOCKET NUMBER: 5789-3
; TELEPHONE: 919 420 2205
; TELEFAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
; LENGTH: 5926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DEM-delta"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

RESULT 3
US-09-993-292A-1/C
; Sequence 1, Application US/09993292A
; Patent No. US20020146430A1

GENERAL INFORMATION:
; APPLICANT: James E. Galen
; TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF
; PROTEINS
; FILE REFERENCE: US09/993, 292A
; CURRENT APPLICATION NUMBER: US/09/993, 292A
; CURRENT FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: 60/252, 516
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSBC84 Expression Plasmid

US-09-993-292A-1

Query Match 8.8%; Score 145.4; DB 10; Length 6271;
Best Local Similarity 99.3%; Pred. No. 2e-34; Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 CAAGCTTGGCTGTTGGGGATGAGAGAGATTTCAGCTGATACAGATAATCAGA 1566
Db 2571 CCAGCTTGGCTTTCGGGATGAGAGAGATTTCAGCTGATACAGATAATCAGA 2512

QY 1567 ACCGAGAGGCGCTCGATAAACAGAAATTGCGCTGGGGAGTAGGGGGGTCCAC 1626
Db 2511 ACCGAGAGGGCTCGATAAACAGAAATTGCGCTGGGGAGTAGGGGGGTCCAC 2452

QY 1627 TGACCCCCATGCCGAACTCAGAGTGA 1653
Db 2451 TGACCCCCATGCCGAACTCAGAGTGA 2425

RESULT 4
US-09-993-222A-18/C
; Sequence 18, Application US/09993292A
; Patent No. US20020146430A1

GENERAL INFORMATION:
; APPLICANT: James E. Galen
; APPLICANT: University of Maryland
; TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF
; PROTEINS
; FILE REFERENCE: US09/993, 292A
; CURRENT APPLICATION NUMBER: US/09/993, 292A
; CURRENT FILING DATE: 2001-11-23
; PRIORITY APPLICATION NUMBER: 60/252, 516

Matches 190; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

PRIOR FILING DATE: 2000-11-22
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 18
 LENGTH: 8908
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pSECB4sacB vector
 US-09-993-292A-18

Query Match Score 8.8%; Score 145.4; DB 10; Length 8908;
 Best Local Similarity 99.3%; Pred. No. 2.5e-34;
 Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 CAGCTTGCTGTTGGATGAGAAAGATTTCAGCCGTATAAGATAATCGA 1566
 Db 5208 CCAGCTTGGCTGTTGGATGAGAAAGATTTCAGCCGTATAAGATAATCGA 5149

Qy 1567 ACGAGAAGGGCTGTGATAAAACAGAATTGCCCTGGCGCAGTAGCCGGTCCCACC 1626
 Db 5148 ACCAGAAGGGCTGTGATAAAACAGAATTGCCCTGGCGCAGTAGCCGGTCCCACC 5089

Qy 1627 TGACCCCCATGCCGAACCTCAAGACTGAA 1653
 Db 5088 TGACCCCCATGCCGAACCTCAAGACTGAA 5062

RESULT 5
 US-09-360-428-10
 Sequence 10, Application US/09960428
 Patent No. US20020115147A1
 GENERAL INFORMATION:
 APPLICANT: Roche Diagnostics GmbH
 TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokaryoti
 FILE REFERENCE: 5272/00/
 CURRENT APPLICATION NUMBER: US/09/960,428
 CURRENT FILING DATE: 2001-09-21
 NUMBER OF SEQ ID NOS: 22
 SEQ ID NO: 10
 LENGTH: 425
 TYPE: DNA
 ORGANISM: Escherichia coli
 US-09-360-428-10

Query Match Score 8.3%; Score 138; DB 10; Length 425;
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1516 CTGTTTGGCGATGAGAGAAGATTTCAGCTGTATAAGATAAACTCAAGCAGAACG 1575
 Db 1 CTTTTTGGCGATGAGAGAAGATTTCAGCTGTATAAGATAAACTCAAGCAGAACG 60

Qy 1576 CGGTCTGTAAACAGAATTGCTGGGGCACTAGGCCGGTCCACCTGACCCCAT 1635
 Db 61 CGGTCTGTAAACAGAATTGCTGGGGCACTAGGCCGGTCCACCTGACCCCAT 120

Qy 1636 GCGGAACCTCAAGAAGTGAA 1653
 Db 121 GCGGAACCTCAAGAAGTGAA 138

RESULT 6
 US-09-887-576-678
 Sequence 678, Application US/09887576
 PCT No. US201404047A1
 GENERAL INFORMATION:
 APPLICANT: Budworth, P.
 APPLICANT: Brown, D.
 APPLICANT: Chang, H.
 APPLICANT: Zhu, T.
 APPLICANT: Han, B.

RESULT 7

US-09-938-842A-990

SEQUENCE 990, Application US/09938842A

PATENT NO. US2002160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT1300-3

CURRENT APPLICATION NUMBER: US/09/938-842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/1227, 866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264, 647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300, 111

PRIOR FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 60/300, 111

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO: 990

LENGTH: 1179

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-990

Query Match 8.2%; Score 136; DB 9; Length 1179;

Best Local Similarity 50.3%; Pred. No. 6.2e-32; Matches 380; Conservative 0; Mismatches 355; Indels 21; Gaps 1;

QY 671 CAACCGCCGGTTGGCTGAGATCACGAGATCATCGAGATACACTCAACCTCTCAGACGAC 1143

Db 415 CACCGCCGGTTGGCTGAGATCATCGAGATACACTCAACCTCTCAGACGAC 1143

QY 731 GTTATCGAGAGGACATCGAGAGAACGACCATCGGAACACASCATCGGAAAC 730

Db 475 GTTATCGAGAGGACATCGAGAGAACGACCATCGGAACACASCATCGGAAAC 730

QY 791 AAGATGGCGATTGGCTGATTCCTGTTGGACGGCGCTGTGATGGCGAGC 790

Db 535 AGATAGCGGTGCTAGCTCGAGATTCTGATGGCTAGTACGAAAT 594

QY 851 TTGGCGCAATCGGGAGTTGAGTTTGCTACTGTTATGCAACCTGGTGGAGGA 910

Db 595 CTCGGAATCTTGAAGTTAACTCTCATCGTGGTGTCAAGAACCTTGCAAGCGGA 654

QY 911 GAGTTCACTCGAGTCAAATACTCTGTGATGGATTGAGGCATCGGGACGCGAGGA 970

Db 655 GAGATAAAGCAGGCCAGCTTATGTCGCAACCCCTTACACC 693

QY 971 ACGTCTGATTACTATTCGAGAAGCTACTTGAGACTCGTCTTGTGTCAGTC 1030

Db 694 AAGCTCGAGCTACTACTCAAAAGTTCTACAGACACCCCTTACACC 753

QY 1031 TGCAGAGCACTGCGCTTCGGTGTGCTACCGCTGATGTCAGTC 1090

Db 754 ACCAAGAGACTGCGATTTCAGCAGATGTCAGAAGAAATGACAG 813

QY 1091 TACCGAAGGACCTTGTGTTGCAATCCACAATGCGACACATCTCGACTACCGRC 1150

Db 814 TTGGAGAAGATCTGCTCTTCAGATAGTGTGATATTGTTGCTACTCAG 873

QY 1151 TCCCGTACCGACTCTGGTAAGCCCCCGGCGCAGCTCTGGCTCGCCACCG 1210

Db 874 TCGAGAGGACGCTGGAAAGCCACAGSAGTATTGCTAAAGGTACTTAAAGCA 933

QY 1211 CGCGCCCTCTGGCTGGAGCACCAAGCCAGCTGGTCCATATCAAGCGAAC 1270

RESULT 8

US-09-900-575-46

SEQUENCE 46, Application US/09900575

PATENT NO. US2002160358A1

GENERAL INFORMATION:

APPLICANT: Landermann, Solomon

APPLICANT: Revel, Andrew

APPLICANT: Auguste, Christine

APPLICANT: Burlein, Jeanne

TITLE OF INVENTION: FimH Adhesin Proteins and Methods of Use

FILE REFERENCE: 469201-549

CURRENT APPLICATION NUMBER: US/09/900, 575

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US/60/216, 750

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 64

SEQ ID NO: 46

LENGTH: 7416

TYPE: DNA

FEATURE: OTHER INFORMATION: Sequence of Plasmid pCGA126-1

ORGANISM: Artificial Sequence

US-09-900-575-46

Query Match 7.9%; Score 130.8; DB 10; Length 7416;

Best Local Similarity 98.5%; Pred. No. 7.5e-30; Matches 132; Conservative 0; Mismatches 0; Gaps 0;

QY 1512 TTGGCGTTGGGGATGAGAGAGATTCTGGCTGATACGATTAATGAAACCA 1571

Db 2255 TTCCCTGTTGGGGATGAGAGAGATTCTGGCTGATAGATTAATGAAACCA 2314

QY 1572 GAACCGGTGTGATAAACAGATAATGCGCTGGCGCAGTAGCCCGGTGCTCCACCTGACC 1631

Db 2315 GAAGGGGTGTGATAAACAGATAATGCGCTGGCGCAGTAGCCCGGTGCTCCACCTGACC 2374

QY 1632 CCGCGCGACTCA 1645

Db 2375 CCGCGCGACTCA 2388

RESULT 9

US-09-938-842A-1124

SEQUENCE 1124, Application US/09938842A

PATENT NO. US2002160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT1300-3

CURRENT APPLICATION NUMBER: US/09/938, 842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300,111
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO: 1124
 LENGTH: 894
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 US-09-938-842A-1124

Query Match Score 7.3%; Best Local Similarity 54.5%; Pred. No. 2.-7e-27; Matches 242; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 954 CTACGGGACGGAGAAACGTGCAACTTGTGAAAGCTACTTTGAGACTCGCTG 1013
 Db 374 CAACCCGACGGCTTATAGTATGGACTACTACATGCAAGAACMATTATAAGACGGCAT 433

Qy 1014 CCTTGATTGCCAAGTCGCAAGAACGCTTCTGGCTGGCTACGGCTGAGGTTG 1073
 Db 434 CGCTTAATCTCTAACAGTGAAGCTGGCTTGCAGTCACTGGACAACAGCAGAGTTG 493

Qy 1074 CTGATGTCATGCTATGCTTACGGAAAGAACCTGTTGGCATCCAGATECTGGAGACA 1133
 Db 494 CGCTGTTAGCTTGTGACTGGAGATCTGGGTTAGCATCCAAATTAAATAGAGACA 553

Qy 1134 TGCCTGACTACACGGCTCCGGTACCGAACCTGGTAAAGCCGGCTGGAGCAACCTTCAGC 1193
 Db 554 TTCTTGATTTCAGGGCACATCTGCCCTCTCGGAAGGGATCTGTGTCAGATATTGCC 613

Qy 1194 TCGGTCTCGCCACCACGCCGGCCCTCTCGCATGGAAAGCCACAGCCGGCTGGTCCCA 1253.

Db 614 ATGGAGTCATACAGCCAACTTCCTGGATGAAAGCTTCCCAACTACCGGAAG 673

Qy 1254 TGATCAAGCGCAAGTCTCTGCCCAAGGAGCTGTCAGCGGAGTTGGTGCAGA 1313
 Db 674 TTGTGATCAAGTCAAAGTCAAAGCTTGTGAGATGTTGACATCTTGTGGAA 733

Qy 1314 AAGATGATGGATGGAAAGGAGCTTGGCAGAGGACTATGCCCTTGTGGATCTGGCAAG 793
 Db 734 AGAGCAAGGGATAACAGGGCAAGAAATTAGCCATGGAACTTAGCAATCTAGCAGCAG 817

Qy 1374 ATGCAATTGGAGCTTCCGGAA 1397
 Db 794 CTGCAATCGGTCTTACCTGAA 817

RESULT 10
 Sequence 27, Application US/09191020
 Patent No. US20045592A1
 GENERAL INFORMATION:
 APPLICANT: Zyskind, Judith
 APPLICANT: Ohisen, Kari L.
 APPLICANT: Trawick, John
 APPLICANT: Forsyth, R. Allyn
 APPLICANT: Froelich, Jamie M.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
 TITLE OF INVENTION: *Escherichia coli*
 FILE REFERENCE: ELTRIA_001DV1
 CURRENT APPLICATION NUMBER: US/09/912,020
 CURRENT FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: 09-1492,709
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: 60/117,405
 PRIOR FILING DATE: 1999-01-27
 NUMBER OF SEQ ID NOS: 485
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO: 27

LENGTH: 799
 TYPE: DNA
 ORGANISM: *E. coli*
 US-09-912-020-27

Query Match Score 115.4%; Best Local Similarity 99.1%; Pred. No. 1.2e-25; Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1537 GATTTCAGCTGATAACGATTAATCAGAGACGCAAGGGCTCTATAAACAGATA 1596
 Db 475 GCCTTGCGGAGTAGTGGCTGCCACCTGACGATTAATCAGAGACGCAAGGGCTCTATAAACAGATA 534

Qy 1597 GCCTGCGGAGTAGTGGCTGCCACCTGACGATTAATCAGAGACGCAAGGGCTCTATAAACAGATA 1653
 Db 535 GCCTGCGGAGTAGTGGCTGCCACCTGACGAGACGCAACTCGAGAGTGA 591

RESULT 11
 Sequence 999, Application US/09974300
 Patent No. US2002046721A1
 GENERAL INFORMATION:
 APPLICANT: Berk, Randy M.
 APPLICANT: Clausen, Ib Groth
 TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 TITLE OF INVENTION: Expression
 FILE REFERENCE: 10085_500-US
 CURRENT APPLICATION NUMBER: US/09/974,300
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/680,598
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 66/279,526
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 8481
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO: 999
 LENGTH: 927
 TYPE: DNA
 ORGANISM: *Bacillus licheniformis*
 US-09-974-300-999

Query Match Score 4.8%; Best Local Similarity 46.8%; Pred. No. 2.2e-14; Matches 341; Conservative 0; Mismatches 363; Indels 24; Gaps 2;

Qy 694 GGAGATGATCCATGGAGCATCACTCTCCACGAGCTTACGACGCTTCGGAGACAG 753
 Db 221 GGAATTTGATACATATGGCTTGCCTCTGTCATACGAGATCTCATGATGGAGCTGAG 280

Qy 754 ACAGAAACGCCACATCGGAAACCCGGCATTTGGCTGGTGA 813
 Db 281 AAGAGGACAGCGGACAATCAAGCGGAAGTGGGATAACGGGATTGAAATACAGGTGA 340

Qy 814 TTTCMTGTTGGACGGCGCTGTGTCATTTGGCAGGTGGCAATTCGGAGGTGATTGA 873
 Db 341 TTATTTGTCCTCGTCATCTGAGCTGAGCTTGTGGATGAAATTAAACGAAGCCATGA 400

Qy 874 GCTTCTGGCTACTGTATGTTGGCTGGGAGAGTTCATGCAGTGGCTTGGCTGGTGA 933
 Db 401 AATCTTGTCAGGGCATTTGTCGAACCTGTCCTTGAGAAATTGAGAACATAAAGATAA 460

Qy 934 TGTGATGATGGCATGGTGGCTACGGCAAGCTTGTGGATCTATTGAGAA 993
 Db 461 ATATAAT-----ATGGAGAAAATCTGAAACCPATTGAGAG 499

Qy 994 GACTTACTGAGACTGCTGCTTGTGAGCTGTCAGGAGCTGGCTTGTGG 1053
 Db 500 AATCAGGCCAGAGACGACTCTAATGCTGAGCTGGAGCTGTC 559

Qy 1054 TGGTGCCTACGCTGAGGTGCTGATGCTTGTGCTTATGCTTACGGAAAGAACCTTGGTTGGC 1113
 Db 560 TGGTGCCTGAAAACATCTAAACGGTGTACTCTGGTATTATGCGEATGTC 619

QY 1114 ATTCGAGATCGTCGAGCATGCTGACTAACCGCTCGCTACCGACTCGTAAAGCC 1173
Db 620 CTATCAAATTATGATGACATCCCTGATTCACATCAAGAAAAGACTTSCGACA 679
QY 1174 CGCGCGGTGAGACCTTCAGCTGGTCTGCACCGCCCTCTGGATGAGAAGCA 1233
Db 680 TGTGGCAGGGATCTGCTTCAGGGAAATGTCACGCTTCCGGTTATATGACGGAA 739
QY 1234 CCAACGCCGAGCTCGTCCATGATCAGGGCAA - - GTRCTCTAACCCAGGAGCTCA 1290
Db 740 GCGTAGTAAAGCGGCCGTGATTTGGTCAACGGAAACACTCCAGAACAGATCA 799
QY 1291 GCGTGCACGGAGTTGGTCAGAAAAGTGATGGATGGAGAAGGAGGCTTGCGGA 1350
Db 800 GCCAGTGTGAGGGCTGAGAGAAAAGATGCGATGTCAGGGTCACTGTA 859
QY 1351 GGACTATGCCAGAAGGGCTTGATGCAATTGGAGTCCGGAGTGGAGGGAA 1410
Db 860 AATGTTAAACAGGTTTCGAATTGGTGAACAGAACCGATAACGGGCCAC 919
QY 1411 GGCTTGTG 1418
Db 920 CGCACTGG 927

RESULT 12

US-09-815-242-9636
; Sequence 9636, Application US/09915242
; Patent No. US20020061669A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA_01A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9636
LENGTH: 972

QY Match 4.1%; Score 68.2; DB 10; Length 972;
Best Local Similarity 45.8%; Pred. No. 5.9e-11;
Matches 348; Conservative 0; Mismatches 378; Indels 33; Gaps 2;

QY 667 CTGCCAACCGGGTTGGCTGAGATCACCGAGATCATGGAGCATCACTCTCCAGA 726
Db 192 CGGCCACGTGACATTCGCGCTCTGATGAGTTATCCACAGGGACCGCTTACATGTA 251
QY 727 CGAGGGTTATGAGGCTTCGGAGAACAGAACGCCCCATCGGAAACCGCATTCGG 786
Db 252 TGATGTGGTGGATGAACTCTGATATGCGTGGCCCAAAGCGAACGGCAATTCGG 311
QY 787 AACAGAGATGGGATTGCGTGTGATTCTGTTGGACGGGGCCTGTCATGAGC 846
Db 312 TAATGCCCGAACGGTGTGTTGCGACTTTATACCCCGCCCTCACATGATGAC 371
QY 847 GAGGTGCGCAATCGGAGGTGATGACCTTGCAACTTGGTGA 906
Db 372 CAGCTCGGCTCGTTAAAGTGTGAGGTGATGTCGGAGGTCATGIGATTGAGA 431
QY 907 GGGAGAGTTCATGCACTGAAATACTGTTATGATGCGATGATGAGGTCATGGCAGCAA 966
Db 432 AGCGGAAGTGCTGCAATGATGAGACGTCATGGATGAGGTCATGGCAGCAA 1026
QY 967 GAAACGTTGATTACTATTCGAGAAGACTACTTGAGAGATGAGGTCATGGCTGATGAGC 530
Db 475 ---ACCGAGAAATTACATGGGGTCAATTACAGTAACAGGCCCTCTGTCGAGC 530
QY 1027 GTCGTGAGAGCAAGTGCCTCTGGCTGAGGTGTCATGTCAGAACGGTGCA 1086
Db 531 CGCCGCCAGTCTCCGGTATCTGGGTGAGGTGTCAGCTGAGAACAGAAAGGGTGCA 590
QY 1087 TGCTTACGAGGAACTCTGGTTGGCATTCAGATCTCGAGAACATGCTGACTAC 1146
Db 591 GGACATATGGCCGCTACCTTGTGGTAGGGCTTCAGCTATGAGATCTGCTGATTAC 650
QY 1147 CGTCCTCGGTACCGACCTCTGGTAGGCCCGGCTGAGACCTCAGCTGCTGCGAC 1206
Db 651 TGCGACAGGGASCATCTGGTAAATACTGGGTGATGACTCAATGGGAAACCTAC 710
QY 1207 CGCGCGGGCCCTCTCGCATGGAAGCACCCGGAGCTCGTGTCCCCTGATCAAGCGCA 1266
Db 711 CTTACCGTGTCTGACGCCATGCCAGGTAGCCAGAACCTACAGGGATATCCGTA 770
QY 1267 GTTCTCTGACCAGAGACGTGAGCTGAGCTGAGGTTGGTGGAGAAA--- 1316
Db 771 CGCTATTGACAAAGTTAATGGCGTATCTCTGAGACCGGTTGGAGGATGACCA 830
QY 1317 -GIGATGGATGGAGAGGAGGAGGAGCTGCGGAGGGATGCCCAGAGGCGTTGGA 1374
Db 831 CTGCGCTCGCTGGATGGACCGCCCTGAGGAGAACGCGCAAAAGCGGATATC 890
QY 1375 TGCACATTGGAGGAGTCCCGGAGAGGAGCTGGCCAGAGGCGTTGGA 1413
Db 891 CGCGTGCAGATATGCCGATACCCATGGCGTGGAGGC 929

RESULT 13

US-10-040-037-1
; Sequence 1, Application US/10040037
; Patent No. US20020102593A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Jack T.
; APPLICANT: MacDonald, Constance
; APPLICANT: MacDonald, Constantine
; APPLICANT: Gabriele, Joseph
TITLE OF INVENTION: Method for Sequencing Reaction Cleanup
; TITLE OF INVENTION: by Constant Pressure Differential Ultrafiltration
; FILE REFERENCE: MCA-480A
; CURRENT APPLICATION NUMBER: US/10/040, 037
; CURRENT FILING DATE: 2001-10-19
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/154, 448
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 976
; TYPE: DNA

ORGANISM: Escherichia coli bacteriophage lambda
us-10-040-037-1

Query Match 3.9%; Score 64.2; DB 12; Length 767;
Best Local Similarity 95.7%; Pred. No. 8 8e-10;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1457 GATTGGAGCTGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCTGGC 1516
Db 9 GATTGGAGCTGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCTGGC 68

RESULT 14

us-10-013-036-3

; Patent No. US20020128186A1

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jeffrey

; TITLE OF INVENTION: Antimicrobial Polypeptide, Nucleic Acid, and Methods of Use

; FILE REFERENCE: 00-1323H

; CURRENT FILING DATE: 2001-10-30

; PRIOR APPLICATION NUMBER: US/10/013,036

; PRIORITY FILING DATE: 1999-07-27

; PRIOR APPLICATION NUMBER: 08/1871,924

; PRIOR FILING DATE: 1997-06-10

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1323

; TYPE: DNA

; ORGANISM: Streptococcus mutans

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (228)..(782)

; OTHER INFORMATION:

; NAME/KEY: -35 signal

; LOCATION: (177)..(182)

; OTHER INFORMATION:

; NAME/KEY: -10 signal

; LOCATION: (197)..(196)

; OTHER INFORMATION:

; NAME/KEY: RBS

; LOCATION: (218)..(224)

; OTHER INFORMATION:

; SEQ ID NO 3

Query Match 3.8%; Score 61; DB 12; Length 1323;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1454 TGGAAATTGGAGCTGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCTATGCAAGCTT 1513
Db 912 TGGAAATTGGAGCTGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCTATGCAAGCTT 971

RESULT 15

us-09-179-536B-267/c

; Sequence 267, Application US/09179536B

; Patent No. US20020042112A1

; GENERAL INFORMATION:

; APPLICANT: Hubert K ster

; David M. Lough

; Gaobing Xiang

; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY

NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAluliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Disquette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20444
FILING DATE: 06-NOV-1997
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-Sep-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/746,055
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/746,036
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/744,590
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20020042112A1-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 858-587-5360
INFORMATION FOR SEQ ID NO: 267:
TELEX: <Unknown>
SEQUENCE CHARACTERISTICS:
LENGTH: 103 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 267:
US-09-179-536B-267

Query Match Similarity 3.7%; Score 61.6; DB 10; Length 103;
Best Local Similarity 88.2%; Pred. No. 1.7e-09;
Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1454 TAGGAATTGGAGCTGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCTATGCAAGCTT 1513

Db 80 TACGAATTGGAGCTGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCTATGCAAGCTT 21

Qy 1514 GGCTGTATTGGGGAT 1529

Db 20 GGCACTGGTCGTT 5

Search completed: January 16, 2003, 09:42:30
Job time : 96 secs

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result No.	Query Match Length DB ID	Description
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	160.4	Copyright (c) 1993 - 2003 Compugen Ltd.
	152.8	1 nucleic search, using sw model
on:	15865.081	January 16, 2003, 07:25:01 ; Search time 1687 Seconds (without alignments)
title:	US-09-830-111A-1	15865.081 Million cell updates/sec
perfect score:	1653	1 ttttgtgggtcgaaaaggc.....atgcggaaactcagaatgtcaa 1653
sequence:		
scoring table:	IDENTITY_NUC	Gapop 10_0 , Gapext 1.0
searched:	16154066 seqs, 809773376 residues	Maximum DB seq length: 0
st-processing:	Minimum Match 0%	Maximum Match 100%
total number of hits satisfying chosen parameters:	323098132	Listing first 45 summaries
database :	EST:*	EST:*
1:	em_estba:*	1: em_estba:*
2:	em_estthum:*	2: em_estthum:*
3:	em_estin:*	3: em_estin:*
4:	em_estmu:*	4: em_estmu:*
5:	em_estov:*	5: em_estov:*
6:	em_estpl:*	6: em_estpl:*
7:	em_estrc:*	7: em_estrc:*
8:	em_htc:*	8: em_htc:*
9:	gb_est1:*	9: gb_est1:*
10:	gb_est2:*	10: gb_est2:*
11:	gb_htc:*	11: gb_htc:*
12:	gb_est3:*	12: gb_est3:*
13:	gb_est4:*	13: gb_est4:*
14:	gb_est5:*	14: gb_est5:*
15:	em_estfun:*	15: em_estfun:*
16:	em_estom:*	16: em_estom:*
17:	gb_gss:*	17: gb_gss:*
18:	em_gss_inv:*	18: em_gss_inv:*
19:	em_gss_pln:*	19: em_gss_pln:*
20:	em_gss_vrt:*	20: em_gss_vrt:*
21:	em_gss_fun:*	21: em_gss_fun:*
22:	em_gss_mam:*	22: em_gss_mam:*
23:	em_gss_mus:*	23: em_gss_mus:*
24:	em_gss_other:*	24: em_gss_other:*
25:	em_gss_pro:*	25: em_gss_pro:*
26:	em_gss_rnd:*	26: em_gss_rnd:*
27:		27:
		RESULTS
		1 AA901612
		LOCUS NCM3AIT3
		DEFINITION Mycelial Neurospora crassa cDNA clone NM3AI 5, end, mRNA
		JOURNAL AA901612
		COMMENT AA901612
		VERSION 1
		KEYWORDS EST.
		AUTHORS Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L., Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E., Cushing,T., Erratt,A., Flehart,M., Gorman,M., Judson,K., Miller,R., Ortega,J., Pavlova,I., Pereira,J., Todisco,S., Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
		REFERENCE 1 (base 1 to 561)
		SOURCE D.O.
		TITLE Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa
		JOURNAL Fungal Genet. Biol. 21, 348-363 (1997)
		COMMENT 97435549
		Department of Biology
		University of New Mexico
		Castetter Hall, Albuquerque, NM 87131, USA
		Fax: 505-277-3411
		Tei: 505-277-0304

Email: ngp@biology.unm.edu
 Putative HEXAPRENYL PYROPHOSPHATE SYNTHETASE PRECURSOR (HPS)
 based upon BLASTX search. Deposited in GSDB at the National Center
 for Genome Resources with accession GSDB:S:1147848
 Seq primer: T3.

FEATURES source

Location/Qualifiers
 1. .561
 /organism="Neurospora crassa"
 /strain="74-OR23-IV A (FGSC 2489)"
 /db_xref="taxon:5141"
 /clone="NM3A1"
 /clone_1.lib="Mycelial"
 /sex="Mating type A"
 /tissue_type="Mycelium"
 /dev_stage="Mycelium"
 /lab_host="E. coli"

/note="vector: pBluescript SK(-) using the Uni-ZAP XR vector system
 Xba I; 24 sucrose for 24 hours. cDNA directionally cloned
 into pBluescript SK(-) using the Uni-ZAP XR vector system
 (Stratagene, La Jolla, CA)." 109 a 204 C 121 t
 BASE COUNT ORIGIN

FEATURES source

Query Match
 Best Local Similarity 10.0%; Score 165.4; DB 9; Length 561;
 Matches 301; Conservative 0; Mismatches 171; Indels 3; Gaps 3;

Qy 657 ATATCCCTCGCCCTCCAAACCG-CGGTTGGTGGAGATCACCGAGATGATCCATGCCAGCATCA 715
 Db 87 ACATCTCCCTCCAGCGAGCAGCTGGCGAGATCACCGAGATGATCCATGCCCTCG 146

Qy 716 CTCTCTCCAGACGAGGTATGAGCCTTCGAGACAGAGAACGACCATCGAAC 775
 Db 147 CTCTCTCAGACGATGTCATGATCCTCGAGTCCTCGCGCGCGCTCCCGCAAC 206

Qy 776 C-AGGCGATTGGAGAAAGATGGGATTGGCGGATTCCTGGAGCGCGTC 834
 Db 207 CTCGAATACTGGAAACAAGTGGCGCTCTGGCGTGTACTCTCTTGAGCGGCCTC 266

Qy 835 TGTGTCATGGCGAGGTGGCAAATCGCGAGGTGTGAGCTT"GGTACTGTTATGC 894
 Db 267 CGTCGCCCTCGCCCTCGCCAGCGAGTCCTGAGCTTCACCGATATGC 326

Qy 895 AAATCTGGTGGAGGAGCTCAGCAGTGGAA-AATACTGTTGATGATGAGTGGAG 953
 Db 327 CAACATTGTCGAGGGGGAGTTCATCGCTCAAGAACAGGGCTCGAGAAAGAAC 386

Qy 954 CTAGGGCAGGAGAAACTGTCGTTACTATTCAGAGACTACTGAGAGCTGGCT 1013
 Db 387 CCCAAATGTCGAGGGAGTCTCCTACTACTCCAAAGAACCTAACCTAACCGCT 446

Qy 1014 CCTCTGATGCCAATGTTGAGAGAAGTGGCTCTGGGGGAGCTGATGGGGACGG 1073
 Db 447 CCTCTGATGCCAAGACTGTCGGCTCTGGCTCTGGGGGAGCTGATGGGGACGG 506

Qy 1074 CTGATGCTGTTATGCTTACGGAGGGACTTGGTTGECATCCAGATGTCGA 1128
 Db 507 TGGATGCTGCTACTTGTGTTGGAGAACCTGGCTTCCAGCTGGCT 561

BASE COUNT ORIGIN

Query Match
 Best Local Similarity 9.7%; Score 160.4; DB 14; Length 656;

Matches 363; Conservative 0; Mismatches 288; Indels 21; Gaps 1;

Qy 728 GACCTTATGACACTTCGGAGGCCAGCGAACGACCATCCGGAAACCAGCATCGGA 787
 Db 1 GATGTTATGGAGATGCTGATAGAGGTTGGGATGGATCTTAACTTCTTATAGGA 60

Qy 788 AACAGATGGCTTGGCTGTGATTCCTGTTGGACGGGGTGTGTCATGGG 847
 Db 61 ATAAGCTTGGAGATGGCTGGATTTCTGTTCTAGAGCTTGTATAACCTCGCC 120

Qy 848 AGTTGGCAATCGGGATGTTGGGTTGGCTACTGTTATGGAACTTGGTGG 907
 Db 121 TCTTTAAACACAGAGTTATCACTAAATAGCAAGCTGTGGGATGGGCTTGTGACA 180

Qy 908 GAGAGTTGATGCTGGCTGAAAAATACTGTTGAGTATGGCTGGGAGCGCAG 967
 Db 181 GGTAAACATGGCAATGACCTACCGACGAGCTGT----- 222

RESULT 2
 BQ994487 BQ994487 656 bp mRNA linear EST 21-AUG-2002
 LOCUS BQ994487_yg_ab1 OG_EFGH1 lettuce serriola Lactuca sativa cdna clone
 DEFINITION OG/F7F20 mRNA sequence.

ACCESSION BQ994487 VERSION BQ994487.1 EST: BQ994487.1 GI:22414022
 KEYWORDS SOURCE lactuca sativa.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;

REFERENCE
 1 (bases 1 to 656)
 AUTHORS
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Risseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositeae Genome Project
<http://compgenomics.ucdavis.edu/>
 Unpublished (2002)

COMMENT
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Arnundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-752-9659
 Fax: 1-(530)-752-9659
 Email: akopik@atgc.org [michelmore@verizonmail.ucdavis.edu]
 singleton, see <http://cgpdb.ucdavis.edu/> for details.
 Plate: QSF; Row: F Column: 20.

FEATURES source

Location/Qualifiers
 1. .656
 /clone lib="QSF2"
 /lab host="E. coli"
 /note="Vector: pBRCDNA5f1B; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdb.ucdavis.edu/> TAG_LIB=QSF_EFGH1 lettuce serriola TAG_TISSUE=flowers pre-fertilized TAG_SEQ=GCTTGACGGG" 195 a 125 c 152 g 182 t 2 others

BASE COUNT ORIGIN

Query Match
 Best Local Similarity 5.4%; Score 160.4; DB 14; Length 656;

Matches 363; Conservative 0; Mismatches 288; Indels 21; Gaps 1;

Qy 728 GACCTTATGACACTTCGGAGGCCAGCGAACGACCATCCGGAAACCAGCATCGGA 787
 Db 1 GATGTTATGGAGATGCTGATAGAGGTTGGGATGGATCTTAACTTCTTATAGGA 60

Qy 788 AACAGATGGCTTGGCTGTGATTCCTGTTGGACGGGGTGTGTCATGGG 847
 Db 61 ATAAGCTTGGAGATGGCTGGATTTCTGTTCTAGAGCTTGTATAACCTCGCC 120

Qy 848 AGTTGGCAATCGGGATGTTGGGTTGGCTACTGTTATGGAACTTGGTGG 907
 Db 121 TCTTTAAACACAGAGTTATCACTAAATAGCAAGCTGTGGGATGGGCTTGTGACA 180

Qy 908 GAGAGTTGATGCTGGCTGAAAAATACTGTTGAGTATGGCTGGGAGCGCAG 967
 Db 181 GGTAAACATGGCAATGACCTACCGACGAGCTGT----- 222

Qy 968 GAAACGTTGATGACTATTGGAGAACTTCTGAGACTGGCTCTGTGATGGCCAAG 1027
 Db 223 - - AGCATGTTGATTAATGCTTGTGAGCTTATACAGACTGTCATTTAAATTCAC 279

Qy 1028 TCTGACGAGCAACTGGCTTGTGGTGTGAGCTGAGGTGTGATCTGCT 1087
 Db 280 AGCTGCAATTCATGACTTCTACGGCCAACTACTGAGGTGTCATGGCAT 339

Qy 1088 GCTTACGGAGGAACTTGGTGTGCACTTCGAGATCGTGGAGCATGTCCTACAC 1147
 Db 340 GAAATGGAAAATCTGGTGTGGCATTCATTAATGATGAGCTACTTCACT 399

Qy 1148 GTCTCGGTACCCACCTGGTAAGCCGGTCAAGCTCAGCTGGTTGCCACC 1207
 Db 400 GGCACATCATCATCTCTAGGAAAGGGTCATPATCTGACATTACCATGGAAATTGACA 459

Qy 1208 GCGCGGCCCTTCGATGGAAAGCACCCAGGGAGCTCGGCCATGATCAGTCAGCTGGCAAG 1267
 Db 460 GTCCAATTATTAATGCRATGGAGGTTCCGAACACTGACAGTGTCCACAGGGC 519

Qy 1268 TCTCTAACCCAGAGCTGGTCAACGGAGCTGGTGGAGAAAGTCATGGATTG 1327
 Db 520 TCGATGACCCCTAAACGTGAACTCTGCTCTCGAGATCTGGATA 579

Qy 1328 GCGAAGACGAGCCCTGGGGAGTGGGAGGATGGCCAGATGGCACTGGACG 1387
 Db 580 CNAAGAACAGAACTGGCAGAACATGGCCAGCTGGCATCTGTCATTTGATCA 639

Qy 1388 TTCCGGAGAGT 1399
 Db 640 TGGCTGAAAT 651

RESULT 3
 CNS06X9P/C CNS06X9P 843 bp DNA linear GSS 06-JUL-2001
 DEFINITION T3 end of clone AX00A039R06 of library AX00A from strain CBS 7064
 of *Pichia farinosa*, genomic survey sequence.
 ACCESSION AL419459
 VERSION GI:12202637
 KEYWORDS GSS
 SOURCE
Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctales; Saccharomycetaceae; Pichia.
 REFERENCES (bases 1 to 843)
 AUTHORS Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Bottlier, P., Casaregola, S., Durrans, P., Llorente, B., Malpertuy, A., Neuvelise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekiai, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P., and Weissenbach, J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876
 REFERENCES (bases 1 to 843)
 AUTHORS de Montigny, J., Spehnner, C., Souciet, J., Tekiai, F., Dujon, B., Wincker, P., Artiguenave, F., and Potier, S.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*
 JOURNAL FEBS Lett. 487 (1), 87-90 (2000)

RESULT 4
 BI722198 LOCUS 690 bp mRNA linear EST 19-SEP-2001
 DEFINITION 1031060E05.Y1 C. reinhardtii CC-1660, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
 ACCESSION BI722198
 VERSION BI722198.1 GI:15697893
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
 REFERENCES 1 (bases 1 to 690)
 AUTHORS Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Leebvre, P., McDermott, J.P., Shrager, J.J., Sifflow, C., and Stern, D.
 TITLE Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
 JOURNAL Unpublished (2001)
 COMMENT Contact: Charles Hauser
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000
 Tel: 919 613 8159
 Fax: 919 613 8177

FEATURES source
 1..843
 /organism="Pichia farinosa"
 /strain="CBS 7064"

Db	475	GAGATGTGACAGAGCACAGCATGATGATTACAGACAGTATGGCTGCAGCAACACT	534	Db	183	ACTTGGAACACAGAGGTGTTCTCTAATGCACTGCACTGCTGTAGAACATCTACTTG	242
Qy	1341	CCCTTGGCGAGGATGATGCCACAGAGCGTTGATGCAATTGGACCTTCGGGAGTC	1400	Qy	910	AGAGTCATGGAGTGAAATACTGTGATGTCGATGAGGCTAGGGCGAGCGAGA	969
Db	535	ACCTCGCCAGTAGTACTGCCACAAGTGAGAGATCAGGAGCTAGACATCTCA	594	Db	243	TGAACATATGCGATCTCACAAAGCAGAGA-----GCAACGGCGAGCATG-	288
Qy	1401	CGGCCACGGAGGTTGGAGCATT 1425		Qy	970	ACGTTGAGATRACTATTGAGAAGACTTACTTGAGAGACTGCGTCCTGATTCAGTC	1029
Db	595	CAGAAAGGACGCCCTATTCACT 619		Db	289	- - - - - GAGTACTACTGAGAAGCATACTACAAACGGCATATGATCAATAG	341
RESULT	7			Qy	1030	CTGAGAGCAGTSGCGCTCTGGTGTCTACCCCTGGGTGCTGATGCTGCTTATG	1089
BQ295774		BQ295774 1091-02F12_y1 1091 - Immature ear with common ESTs screened by	597 bp mRNA linear EST 16-MAY-2002	Db	342	TGCAAGGCTGTGCTATCTGCAGGGCACACACTGAGGCTGGCTTGCTCATATGA	401
LOCUS		Schmidt lab Zea mays cDNA, mRNA sequence.		Qy	1090	TACGGAAAGGACCTGGTTGGATTCAAATGCTGACGAGCATGCTGACTACACGT	1149
DEFINITION				Db	402	ATATGTCGAAACCGGGCTAGCTCAGTTAATGATGATGATGTTGATTCACGG	461
ACCESSION		BQ295774		Qy	1150	CTCCGGTACCGACCTCGGTAGACCCGGCTCGACAGCTCCGCTCGGACCGC	1209
VERSION		BQ295774.1 GI:20811296		Db	462	ACCTCTGCAATCCCTGGAGGGTCATGTCGATATTGCCACGGATTACGCC	521
KEYWORDS		Zea mays.		Qy	1210	GCCGGCCCTCTGATGAGACACCACCCGAGCT 1245	
SOURCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Bilipsida; Poales; Poaceae; PACC		Db	522	CCCGATGCTATATGCGATGGAGGAATTCCCACACT 557	
REFERENCE		1 (basee 1 to 597)		FEATURES		RESULT	8
AUTHORS		Walbot, V.		source		AL582288/c	
JOURNAL		University		1. Location/Qualifiers		AL582288	
COMMENT		Unpublished (1999)		1. . 597		LTI_NFL010_BC2	949 bp mRNA linear EST 16-FEB-2001
AUTHORS		Department of Biological Sciences		1/organism="Zea mays"			prime mRNA sequence.
TITLE		Stanford University		/cultivar="O'H43"			
		855 California Ave, Palo Alto, CA 94304, USA		/db_xref="txon:4577"			
Fax:	650 723 2227			/clone_lib="1091 - Immature ear with common ESTs screened			
Email:	walbot@stanford.edu			by Schmidt lab"			
Plate:	1091042 row: F column: 12.			/tissue_type="Inflorescence meristem - floral organ			
FEATURES		Maize ESTs from various cDNA libraries sequenced at Stanford		primordia"			
source				/dev_stage="0.5 cm to 2 cm"			
				/lab_host="Stratagene X10R"			
				/note="Organ: Immature ear; Vector: pAD-GAL4; Site: 1:			
				EcoRI; Site: XhoI; RNA from library 606 was filtered for			
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BASE COUNT	155 a 125 C 148 G 169 t			FEATURES			
ORIGIN				source			
Query Match	8.5%	Score 141.2; DB 14; length 597;		1. Location/Qualifiers			
Best Local Similarity	55.9%	Pred. No. 1.5e-26;		1. . 949			
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Qy	670	GCAGGGCGTGGCTGAGATCAGGAGATGACCATGAGCTACCTCTCCAGGAGA	729	/db_xref="Taxon: 9606"			
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Db				/note="Vector: pCMVSPORT 6; Site: 1; NotI; 1st strand cDNA			
Qy	790	CAAGATGGGATTGGCTGGTGTGTTCTGTTGGAGGGCTCTGTCATGGAG	849	was primed with a NotI-oligo(dT) primer. Five prime end			
Db	123	CAAGCTTCTGCTGCTGCTGATCTCTCTGAGCTGATGCTGCTGAGCTG	182	enriched, double-stranded cDNA was digested with Not I and			
Qy	850	GTGGCGCATCCGAGGAGTGAACCTTGACTGATCTGATTCACCTGGAGG	909	cloned into the Not I and Eco RV sites of the pCMVSPORT 6			
				vector. Library was normalized. Library was constructed by			
				Life Technologies. Contact: Feng Liang Life Technologies,			
				a division of Invitrogen 9800 Medical Center Drive			
				Rockville, Maryland 20850, USA Fax : (1) 301 610 8371			
				Email : fliang@lifetech.com URL :			
				http://fulllength.invitrogen.com"			
BASE COUNT	285 a 192 C 185 G 283 t 4 others			ORIGIN			
Query Match	8.3%	Score 137; DB 9; Length 949;					
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Matches	354;	Conservative 1; Mismatches 311; Indels 21; Gaps 1;					
Qy	781	ATTGGAAACAGATGCGATTGGCTGATTCCTGTTGGAGCGGGCTGTC	840				

QY	1338	GAGCTTGGGGAGGAGTA	1356	BG252364	897 bp	mRNA	linear	EST 13-FEB-2001	RESULT 10
Db	580	CCTACTCGCCACAGCTA	598						
FEATURES									
SOURCE									
ORGANISM		Homo sapiens							
REFERENCE	1	(bases 1 to 897)							
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/							
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)								
JOURNAL	Unpublished (1999)								
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov								
TISSUE	Procurement: ATCC								
CDNA Library Preparation:	Life Technologies, Inc.								
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)								
DNA Sequencing by:	Incyte Genomics, Inc.								
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov								
Plate:	LLAM0297	row: n	column: 13						
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AUTHORS	/lab_host="BHL10B (phage-resistant)"								
TITLE	/note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."								
BASE COUNT	255	a	194	c	197	g	251	t	
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Db	17	CAGCTTAATAGATCTGGGGTGAAAGAGCTGGCTCTGGGATTTAATTCCTG	76						
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Db	77	CAGCACTTCTAGCTCTGGGACGAAATTGGAAATACGTTATCTATTTAACCCAAG	136						
QY	888	TTATGCAACTTGTGGGGAGGTCTATGCACTGCTGAA	947						
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Db	192	-----GAGTGAAGATTGCACTACCTTGAGAGACTTACTGAA	235						
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Db	236	CCGGCAGCCTGATGCCAACAGTGTAAAGCACTGCTCTGCTAGATGCCACCG	295						
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REFERENCE
 AUTHORS van der Hoeven, R., Bezzerezides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tansley, S.
 TITLE Generation of ESTs from tomato shoot/meristem tissue
 JOURNAL Unpublished (2001)
 COMMENT Contact: CGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES Location/Qualifiers
 Source J. .735
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
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RESULT 12
 BG125274 LOCUS BG125274 735 bp mRNA linear EST 31-JAN-2001
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 CTOF8K7 5' sequence, mRNA sequence.

ACCESSION BG125274.1 GI:12625462
 VERSION EST.
 KEYWORDS tomato.
 ORGANISM Lycopersicon esculentum
 Sporophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 735)

REFERENCE
 AUTHORS van der Hoeven, R., Bezzerezides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tansley, S.
 TITLE Generation of ESTs from tomato shoot/meristem tissue
 JOURNAL Unpublished (2001)
 COMMENT Contact: CGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

/clone="ctof8k7"
 /clone_id="tomato shoot/meristem"
 /tissue_type="shoot/meristem"
 /dev_stage="developing shoots from 4-6wks old plants"
 /lab_host="ISOLR"
 /note="Vector: pBluescript SK(-); Site: EcoRI; Site: XbaI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old) TA496. Tissue was immediately frozen in liquid nitrogen."
 BASE COUNT 200 a 149 c 168 g 218 t
 ORIGIN
 Query Match Score 133.2; DB 12; Length 735;
 Best Local Similarity 59.1%; Pred. No. 2, 4e-24;
 Matches 259; Conservative 0; Mismatches 158; Indels 21; Gaps 1;
 Qy 682 GGCCTGAGATCAGCGAGATGATCCATGAGCATCACTCCACGAGCGTATTGAGC 741
 Db 278 GGCCTGAGATCAGCGAGATGATCCATGAGCATCACTCCACGAGCGTATTGAGC 337
 Qy 742 TTCCGAGACACAGAACGAAACGACCCATCCGGAAACAGCACATCGGAACAAAGATGGGAT 801
 Db 338 TCCTGAGACAAAGAACGCTGGATAGGGTTCTTAAACTTGTGATGGAAATAAGCTAGCTG 397
 Qy 802 TTGGCTGGTGATTCTGTTCTGGACGGCGCTGTGCAATTGGAGGTTGGCAATCC 861
 Db 398 ACTAGCGGAGACTTTGCTTCCAGGCACTTGCTGAGCAGTTCAGTGGACAATAGAAC 457
 Qy 862 CGAGGGTGAATTGAGCTTITGGCTACTGTATTGCAAACACTTGTTGAGGGAGAGTTCTAGCA 921
 Db 458 AGGGCTGTGATGCTCTGGCAACCTGTTGTTACTTGAGGACAATAGCA 517
 Qy 922 GTTGAAGAAATAACTGTGATGATGGCTACGGCAACGTTGCAATTGAGGCTACGGCAAC 981
 Db 518 AATGAGCAACTCTCTCTGATGA-----ACGTTGTTGAGATGGGAGTA 556
 Qy 982 CTATTGGAGAGACTTCTGAAAGACTGCTGCTCTGATGGCAAGCTGCTGAGGAGAAG 1041
 Db 557 TTAATGGAGAAACATTTACAAGACTGCTATGTTCAAATAGTGCAAAAGCT 616
 Qy 1042 TCGGCTTCTGGCTGCTGAGGTTGCTGATGCTGTTAGCTTACGGAAACGGAA 1101
 Db 617 TGCACTACTTGCTGGGATTAAGTGTGCTGAGTGGCTACGGTTGAGCTACGGAAAAAA 676
 Qy 1102 CCTTGTTTGGGATTCGA 1119
 Db 677 TCTGGGATGGCATTTCA 694

RESULT 13
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 DEFINITION Zea mays PC0073322 mRNA sequence.
 ACCESSION AY108392
 VERSION AY108392.1 GI:21211470
 KEYWORDS HTC.
 SOURCE Zea mays.
 ORGANISM Zea mays
 REFERENCES 1 (bases 1 to 1112)
 AUTHOR(S) Arthur, L.W., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Rainey, C.F., Hanafey, M., Morgan, M. and Tingey, S.V.
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
 JOURNAL Unpublished (2002)
 REFERENCE 2 (bases 1 to 1112)
 AUTHOR(S) Coe, E.C.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 FEATURES Location/Qualifiers

FEATURES	SOURCE	COMMENT	SEARCHED	LOCATED	QUALIFIERS
RE858032	Chlamydomonas reinhardtii	Unpublished (2000)	Qy	670 GCAACGGGGTTGGCTGAGATACGGAGATCCATGCAGCATCCTCACCGAGCA 729	
LOCUS	BG858032	Contact: Charles Hauser	Db	125 GCACCGGGACTTGCAGATTACCGAGAAAGCACCATTCCGGAAAATTCGAAA 184	
DEFINITION	659 bp mRNA linear	Duke University	Qy	730 CGTTATGACGCTTCGGAGAACAGAACATCCGGAAAATTCGAAA 789	
ORGANISM	1024055D07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II	Durham, NC 27708-1000	Db	185 CGTGTGACGTGCCAATCGGCAAAAGCTCAC 244	
VERSION	BG858032	Tel: 919 613 8159	Qy	790 CAAGATGGGATTTGGCTGTTGATTCTTGACGGCGCTGTTGATTGGCGAG 849	
KEYWORDS	1 GI:14239216	Fax: 919 613 8177	Db	245 CGCGTGCGCCGCTGGCTGGCGGACTTCCTGTTGCCAGTTCCTGCCAA 304	
SOURCE	Chlamydomonas reinhardtii	Email: chause@duke.edu	Qy	850 GTTGCAGAATCGGAGGTGATTGAGCTTTCGGCTACTGTTGAGGG 909	
ORGANISM	Chlamydomonas reinhardtii cdDNA, mRNA sequence.	Location/Qualifiers	Db	305 CCTGGACAACCTGGAGTTCATCAAGTGTATGTCAGTCAAGTGTATGGCACTTGGCAACGG 364	
REFERENCE	1 (bases 1 to 659)	Job time : 1707 secs	Qy	910 AGAGTTCATGGAGTTGAAAAAAATACTGTTGATGCGATGAGGCTACGGGACGGAGGA 969	
AUTHORS	Grosman,A., Davies,J.J., Federpel,N., Harris,E., Lefebvre,P.,	Search completed: January 16, 2003, 08:51:38	Db	365 CGAGATCGCCGCGCAGCGCTGTTGACCGACAT 403	
TITLE	McDermott,J.P., Silllow,C., Stern,D. and Surzycki,R.		Qy	970 AACGTTGATGAGTACTATTGGAGAAGACTTGGAGACTTGGCTCTTGTATTGCCAAAGTC 1029	
JOURNAL	Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2		Db	404 CACTCTGGAGCAGTACCTGGCAAGTGTCTACAGAGCCGCTTCGTCATGCCGCAG 463	
COMMENT	Unpublished (2000)		Qy	1030 GTGCAGAGCAAGTGGCTTCGGCTGGCTGAGTTGCTGTAATGC 1089	
	Contact: Charles Hauser		Db	464 CTGGCGCTCCGCCGCGCTGGTCAAGGACGCTGNGAGGTGAAGAGGCCATGTAGCGC 523	
	DCMB Box 91000		Qy	1090 TTACGGAGGAACCTTGGTTGGCATTCGAGTCGACTACACGT 1149	
	Duke University		Db	524 CTACGGCAAGCACCTGGCTGGCATTCGAGTCGACTACGGCACTTGGACTTCAGCA 583	
	Durham, NC 27708-1000		Qy	1150 CTCCGGTACCCACCTGGTAAGCCGGGTGAGCCCTCCAGCTGGCCACCGC 1209	
	Tel: 919 613 8159		Db	584 AACCAAGGGAGCTGGCAAGCCGAGGACCTTGGCAACCTCAGCGC 643	
	Fax: 919 613 8177		Qy	1210 GCGGGCCCTCTPICGC 1224	
	Email: chause@duke.edu		Db	644 GCCCGTCACTCTTCGC 658	
	1. 659				
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	/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XbaI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO ₂ and HS medium bubbled with 5% CO ₂ . PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI ('5') and XbaI ('3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."				
BASE COUNT	133 a	Score 125.4; DB 12; Length 659;			
ORIGIN	213 c	Pred. No. 2.7e-22; Mismatches 236; Indels 21; Gaps 1;			

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